Perfect score:

Sequence:

Searched:

Database

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Sequence 2, Appl1
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Sequence 3, Appl1
Sequence 2, Appl1
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Sequence 4, Appl1
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    DB 6; Leny
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Sequence 2, Application US/08981088
Eatent NO. 6146824
GENERAL INFORMATION:
APPLICANT: BAR-SHAVIT, RACHEL
APPLICANT: BAR-SHAVIT, RACHEL
TITLE OF INVENTION: ANTI-METASTATIC AND ANTI-ANGIOGENIC
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESSE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Carney, Darrell H.; Glenn, Kevin C.
TITLE OF INVENTION: THROMBIN DERIVED POLYPEPTIDES; COMPOSITIONS AND METHODS FOR USE
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/925,201
FILING DATE: 31-OCT-1986
              US-07-720-189-1
US-09-665-872-2
US-09-667-570A-2
US-09-667-570A-1
US-08-295-411-1
US-08-955-411-1
US-08-955-411-1
US-08-955-411-1
US-08-955-411-1
US-08-955-411-1
US-08-955-411-1
US-08-955-411-1
US-08-756-506-4
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s; Pred. No. 0.0C
0; Mismatches
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5225537-2
5270178-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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;Patent No. 5352664
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STATE:
SEQ ID NO:3
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                                                                                                                                                               May 12, 2003, 15:33:37 ; Search time 9.6 Seconds (without alignments) 30.649 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, 7
Sequence 52,
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Sequence 5
Patent No.
Patent No.
Patent No.
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Sequence 1
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Sequence 8
Sequence 2
Sequence 6
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/cgn2_6/ptcdata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptcdata/1/1aa/6A_COMB.pep:*
/cgn2_6/ptcdata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptcdata/1/1aa/PCTUS_COMB.pep:*
/cgn2_6/ptcdata/1/1aa/PCTUS_COMB.pep:*
                            GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-338-364-8

US-08-338-368-2

US-08-558-269-10

US-09-410-882-10

US-09-410-82-10

US-09-955-471-4

US-09-955-471-4

US-09-972-11

US-09-972-1

US-09-518-06-25

US-09-518-06-25

US-09-518-06-25

US-09-518-06-25

US-09-518-06-25

US-09-952-37-3

US-09-952-37-3

US-09-96-00-3

US-09-96-00-3

US-09-96-00-3

US-09-96-00-3

US-09-90-00-3

US-09-90-00-3

US-09-90-00-3

US-09-90-00-3

US-08-944-483-51
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5270178-20
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         protein search, using sw model
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Gapop'10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                          US-09-909-348-1
59
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Match Length
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Gaps

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ZIP: 94404
            ADDRESSEE:
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                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: CAREY, DARRELL H.
APPLICANT: RAMARKISHNAN, SHYAM
TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS
FILE REFERENCE: CHBP:002
CURRENT APPLICATION NUMBER: US/08/330,594C
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial, Sequence: Synthetic OTHER INFORMATION: Peptide
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Pred. No. 0.0039;
                                                                                                                                                                                                                                                                                            Mismatches
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REGISTRATION NUMBER: 27,075
REFERENCE/DOCKET NUMBER: JAO 40455
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GRANADOS, EDWARD N.
KLASS, MICHAEL R.
RUSSELL, JOHN C.
STEWART, KENT D.
STROUPE, STEVEN D.
NVENTION: NOVEL SERINE PE
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08330594C Patent No. 6184342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 52, Application US/08944483 Patent No. 6232456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                               TELEPHONE: (703)-836-6400
TELEFAX: (703)-836-2787
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1994-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                                       23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                           peptide
NO
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                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: pept; HYPOTHETICAL: NO US-08-981-088-2
                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                      1 CEGDSGGPFV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-330-594-8
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APPLICANT:
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100.0%; Score 59; DB 4; Length 259; 100.0%; Pred. No. 0.038; Live. 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,368
FILING DATE: HANOV-1994
CLASSIFICATION: 435
                                                                                                                                                    OPERATING SYSTEM: DOS
SUFTWARE: Fastsep for Windows Version 2.0
SURTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: GILEAD SCIENCES, INC. 353 LAKESIDE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: GIBBS, CRAIG S.
APPLICANT: LEUNG, LAWRENCE L.K.
APPLICANT: TSIANG, MANUEL
TITLE OF INVENTION: NOVEL POLYPI
TITLE OF INVENTION: THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                           NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 6
ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: No. 6232456e
US-08-944-483-52
                                                                                                                          IBM Compatible
                                                                                                                                                                                                                                                                                                                                     TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                             Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 847/935-17
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                               ZIP: 60064-3500
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
Abbott Park
                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOSTER CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                   FILING DATE:
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318 CEGDSGGPFV 327

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Serine Protease-Derived Polypeptides and Anti-Peptide Antibodies, Systems and Therapeutic Methods for Inhibiting Coagulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Griffin, John H.
APPLICANT: Mesters Rolf M.
TITLE OF INVENTION: Serine Protesse-Derived Polypeptid
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems a
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: ADDRESSE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
ADDRESSEE: Research Institute
ADDRESSEE: Research Institute
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                                                                                          GENERAL INCORMATION:
APPLICANT: Crea, Roberto
TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS
TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS
OCRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 59; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: US 07/847,800
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII (text)
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/09/410,882
                                 US-09-410-882-10
; Sequence 10, Application US/09410882
; Patent No. 6287561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08295411
Patent No. 5679639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,709 REFERENCE/DOCKET NUMBER: CR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                     COUNTRI.

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
TIBM PC COMPATID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 376 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-09-410-882-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (617)
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318 CEGDSGGPFV 327
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
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STATE:
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                                                                                                                                                                                                                                                                                                Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Crea, Roberto
ATTLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                  100.0%; Score 59; DB 3;
100.0%; Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CRI-001CP2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,269
FILING DATE: 13.NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,800
FILING DATE: 06-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08558269 Patent No. 5961973
ALIGNEL TREAT TO ANY D.
REGISTRATION NUMBER: 27,043
REFERENCE/DOCKET NUMBER: 190.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-574-899
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P
                                                                                                                                                                  LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-338-368-2
                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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237 CEGDSGGPFV 246
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STATE: MA
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COUNTRY:

RESULT 6 US-08-558-269-10

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1 CEGDSGGPFV 10

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100.0%; Score 59; DB 2; Length 579; 100.0%; Pred. No. 0.081;
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Patent No. 6060300
GENERAL INFORMATION:
APPLICANT: RADITSHC, Martin; FRIEDRICH, Thomas;
APPLICANT: HOLESGHWEILER, Claus; SCHMIDT, Martin;
APPLICANT: HOEFFKEN, Hans Wolfgang; SCHWEDEN, Juergen;
APPLICANT: and RUEBSAMEN, Klaus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Prothrombin Heavy Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Prothrombin Light Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombin muteins as antidote for thrombin inhibitors
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                                   CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LEMCTH: 579 amino acids
TYPE: amino acids
TYPE: amino acids
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                     US/08/955,471
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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TITLE OF INVENTION: thre
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Region
LOCATION: 1.320
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: prof
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Best Local Similarity
Matches 10; Conserv
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STREET: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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Anti-Peptide Antibodies, Systems and Therapeutic Methods
for Inhibiting Coagulation
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ADDRESSEE: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC
CITY: La Jolla
                                                                                                    COFTWARENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-Aug-1994
CLASSIFICATION DATA:
PRUICATION NUMBER: US/08/295,411
FILING DATE: 12-Aug-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNET/AGENT INFORMATION:
NAME: FILLING, Thomas
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELEPHONE: 619-554-2937
TELEPHONE: 619-554-2937
FELEFAX: 619-554-2937
FELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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Pred. No. 0.081;
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                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 5968751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
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Best Local Similarity 100.0%;
Matches 10; Conservative 0
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Rolf M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Region
LOCATION: 321..579
CTHER INFORMATION:
US-08-295-411-4
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Griffin,
APPLICANT: Mesters,
                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Region
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US-08-955-471-4
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Length 615;
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                 Indels
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Patent No. 5502034
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: FOSIEr, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      ADDRESSE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentieth Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,972A FILIG DATE: 19921230 CLASSIFICATION: 435
Pred. No. 0.081;
; Mismatches 0;
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Pred. No. 0.086;
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APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PAITMENER: 31,990
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-12-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                      Sequence 3, Application US/07998972A Patent No. 5476777
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100.08;
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LENGTH: 615 amino acids
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 Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 10; Conserv
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                                                                            1 CEGDSGGPFV 10
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94105
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                                                                                                                                                       RESULT 12
US-07-998-972A-3
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Anti-Peptide Antibodies, Systems and Therapeutic Methods
for Inhibiting Coagulation
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                                                                                                                                                           Length 579;
                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Prothrombin Heavy Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: Office of patent Counsel, The Scripps SSEE: Research Institute
Is 10666 North Torrey Pines Road, TPC 8
La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                           100.0%; Score 59; DB 3; 100.0%; Pred. No. 0.081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                  PCT-US92-10242-4.
; Sequence 4, Application PC/TUS9210242; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
TELEFAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 579 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                MOLECULE TYPE: protein
; ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-117-708-14
                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: Region
; LOCATION: 321..579
; OTHER INFORMATION:
pcr-US92-10242-4
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Griffin, J
APPLICANT: Mesters, R
TITLE OF INVENTION: S
TITLE OF INVENTION: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Region
                                               linear
                                                                                                                                                                                                                                                                           521 CEGDSGGPFV 530
             amino acid
                                                                                                                                                                                                                                     1 CEGDSGGPFV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
STREET: 10
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Gaps

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Length 579;

DB 5;

100.0%; Score 59;

Query Match

CORRESPONDENCE ADDRESS:

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Length 615;
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APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentieth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                             FILING DATE: 30-DEC-1992
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
ANDR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,990
REFERENCE/FOCKET NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTONNEY/AGENT INFORMATION:
NAME: PARMELE, Steven W
REGISTRATION NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 13952-12-2 FELECOMMUNICATION INFORMATION: TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11357
FILING DATE: 19921230
           US 07/998,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application PC/TUS9211357 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                       1: 615 amino acids
amino acid
XX: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 10, Conservative
                                                                                                                                                                                                                                                                                         TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-462-261-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            San Francisco
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557 CEGDSGGPFV 566
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PCT-US92-11357-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: Townsetteth Flaza, Stewart Street Tower,
STREET: Twentieth Floor
GITTY: San Francisco
ADDRESSEE: Townsend and Townsend STREET: One Market Plaza, Stewart Street Tower, STREET: Twentleth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94105
COMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
-SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/463,953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08462261
Patent No. 5527692
GENERAL INFORMATION:
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 135
TELECOMMUNICATION:
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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557 CEGDSGGPFV 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-08-462-261-3
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STATE:
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us-09-909-348-1.rai
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; TYPE: AMINO ACID ; TOPOLOGY: linear ; MOLECULE TYPE: protein PCT-US92-11357-3

0; Gaps Query Match 100.0%; Score 59; DB 5; Length 615; Best Local Similarity 100.0%; Pred. No. 0.086; Matches 10; Conservative 0; Mismatches 0; Indels (

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1 CEGDSGGPFV 10 |||||||||||| 557 CEGDSGGPFV 566 ò

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Search completed: May 12, 2003, 15:40:35 Job time : 10.6 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 12, 2003, 15:33:02 ; Search time 11.4 Seconds (without alignments) 84.328 Million cell updates/sec

US-09-909-348-1 59 1 CEGDSGGPFV 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched: 283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

piri:* pir2:* pir3:* PIR_73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	_	Ĭ	_	·	_	٥	~	_	_	thrombin (EC 3.4.2	thrombin (EC 3.4.2	hepsin (EC 3.4.21.	polyprotein - Afri	9		protein C (activat		cal			_	hypodermin C (EC 3	serine proteinase	chymotrypsin-like	utsc	ည <u>ှ</u>	1ke	ike	trypsin-like prote
																								•					
£	F42696	D42696	E42696	H42696	C42696	142696	G42696	S10511	A35827	TBHU	TBBO	S00845	T30337	845356	KXBO	KXHU	S49323	T15451	146712	184621	JQ0419	A27802	PS0049	A23473	KYVH2C	S68702	TRWV5Y	TRWV3Y	S65465
82	7	~	N	~	~	7	7	~	~	ч	-	٦	~	~	-	Н	7	~	~	7	7	~	7	~	-	7	-	Н	~
s Query Match Length	234	235	235	235	236	236	239	617	618	622	625	417	1524	225	456	461	248	265	275	282	459	230	61	126	218	237	238	254	254
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	94.9	Ψ.	83.8	89.8	89.8	88.1	88.1	88.1	88.1	88.1	86.4	84.7	84.7	84.7	84.7	84.7	84.7	84.7
Score	59	29	59	59	59	29	59	59	59	59	50	26	26	53	53	53	52	52	52	52	52	51	20	20	20	20	20	50	20
Result No.	-	N	9	4	Ŋ	φ	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

1 CEGDSGGPFV 10

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trypsin-like prote neuropsin - mouse chymotrypsin-like trypsin-like prote trypsin (EC 3.4.21 mast cell tryptase serine proteinase tryptase (EC 3.4.21 trypsin (EC 3.4.21 tryptase (EC 3.4.2	tryptase (EC 3.4.2
TRFF 156559 138136 538136 540006 541308 541308 747246 535339 540007 540005 835863	C35863
ничичичичичи	7
256 266 267 267 271 271 271 271 271 271 271 271 271	275
888888888 444888888888 7.7.7.7.4448888888 7.7.7.7.4448888888888	84.7
00000000000000000000000000000000000000	50
6 6 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	45

ALIGNMENTS

RESULT 1 F42.056 thrombin (EC 3.4.21.5) B chain - Cynops pyrogastor (fire-bellied newt) (fragment) C;Species: Cynops pyrogastor (fire-bellied newt) C;Species: Cynops pyrogastor (fire-bellied newt) C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999	C, Accession. 1-2209. R;Banfield, D.K.; MacGillivray, R.T.A. Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Reference number: A42696; MUID:92212913; PMID:1557383	A, Accession: F42696 A, Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A, Molecule type: mRNA A, Regidues: 1-234 (BANA A, Regidues: 1-234 (BANA A, Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology C, Keywords: hydrolase; serine proteinase	Query Match Best Local Similarity 100.0%; Score 59; DB 2; Length 234; Best Local Similarity 100.0%; Pred. No. 0.0092; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 1 CEGDSGGPFV 10 Db 176 CEGDSGGPFV 185	RESULT 2 D42696 thrombin (BC 3.4.21.5) B chain - chicken (fragment) C; Species: Gallus gallus (chicken) C; Species: G-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999 C; Arcasaion: D42696	R.Banfield, D.K.; MacGillivray, R.T.A. R.Banfield, D.K.; MacGillivray, R.T.A. Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992 A,Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A; Ritle: Partial characterization of vertebrate prothrombin cDNAs: amplification and A; Reference number: A42696; MUID:92212913; PMID:1557383	A;Status: preliminary A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-235 <ban> A;Residues: 1-235 <ban> C;Superfamily: thrombus; Gla domain homology; kringle homology; trypsin homology C;Reywords: hydrolase; serine proteinase F;1-226/Domain: trypsin homology (fragment) <try></try></ban></ban>	Query Match 100.0%; Score 59; DB 2; Length 235; Best Local Similarity 100.0%; Pred. No. 0.0093; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Gaps

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RESULT 7

GA2696

thrombin (EC 3.4.21.5) B chain - rainbow trout (fragment)
C; Species: Oncorhynchus mykiss (rainbow trout)
C; Species: Oncorhynchus mykiss (rainbow trout)
C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C; Accession: 642696
R; Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A; Title: Partial characterization.of vertebrate prothrombin cDNAs: amplification and A; Reference number: A42696; MUID:92212913; PMID:1557383
A; Accession: 642696
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-239 <ABNA
A; Cross-references: GB:N81398; NID:9213486; PIDN:AA49433.1; PID:9213487
C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C; Keywords: hydrolase; serine proteinase
F; 1-226/Domain: trypsin homology (fragment) <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Eptatretus stouti (Pacific hagisis) (Ingyment) (C; Species: Eptatretus stouti (Pacific hagisis) (C; Species: Eptatretus stouti (Pacific hagy-1994 #text_change 17-Mar-1999) (C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999) (C; Arressaion: 142696 Marrela (Arrela: Partial characterization of vertebrate prothrombin cDNAs: amplification and Arrela: Partial characterization of vertebrate prothrombin cDNAs: amplification and Arrela: Partial characterization of vertebrate prothrombin cDNAs: amplification and Arrela: preliminary; not compared with conceptual translation Arrestocale type: mRNA Arrestocale translation not given (C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology (C; Superfamily: thrombin; Gla domain homology; Kringle homology; trypsin homology (Frayment) < TRN>
                                                             C;Superfamily: thrombin; Gia domain homology; kringle homology; trypsin homology C;Reywords: hydrolase; serine proteinase F;1-227/Domain: trypsin homology (fragment) <TRY>
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                                                                                                                                                                                              Length 236;
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                                                                                                                                                                                           100.0%; Score 59; DB 2; 100.0%; Pred. No. 0.0093;
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                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombin (EC 3.4.21.5) B chain
                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                   A; Cross-references: GB: M81396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 CEGDSGGPFV 186
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                                                                                                                                                                                                                                                                                                                                                             178 CEGDSGGPFV 187
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Best Local Similarity
Matches 10; Conserv
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C;Species Oryctolagus cuniculus (domestic rabbit)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C;Accession: C42696
K;Banfield, D.K.; MacGilliyray, R.T.A.
Proc. Natl. Acad. Scl. US.A. 89, 2779-2783, 1992
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq A;Reference number: A42696; MUID:92212913; PMID:1557383
A;Accession: C42696
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual transcolube type: mRNA
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Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Itle: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq A;Reference number: A42696; MUID:92212913; PMID:1557383
A;Accession: E42696
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R;Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and sec A;Reference number: A42696; MUID:92212913; PMID:1557383
A;Accession: H42696
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
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C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-226/Domain: trypsin homology (fragment) <TRY>
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C;Superfamily: thrombin, Gla domain homology; kringle homology; trypsin homology
C;Reywords: hydrolase; serine proteinase
F;1-226/Domain: trypsin homology (fragment) <TRY>
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C;Species: Gekko gecko (tokay)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
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C;Species: Acipenser transmontanus (white sturgeon)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C;Accession: H42096
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100.0%; Pred. No. 0.0093;
ive 0; Mismatches 0;
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177 CEGDSGGPFV 186
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A; Residues: 1-235 <BAN>
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thrombin (EC 3.4.21.5) precursor [validated] - human
N;Alternate names: coaqulation factor II
N;Alternate names: coaqulation factor II
N;Contains: prothrombin
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Species: Homo sapie
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A; Residues: 44-118, 'N',120,'S',122-163,'I',165-175,'A',177-182,'T',184-193,'MV',196-3
R; Butkowski, R.J.; Ellon, J.; Downing, M.R.; Mann, K.G.
B. Biol. Chem. 252, 4942-4957, 1977
A; Title: Primary structure of human prethrombin 2 and alpha-thrombin.
A; Reference number: A37550; MUID:77207112; PMID:873923
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A; Residues: 315-334, 'N', 336-348, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 4
R; Rabiact, M.J.; Blashlil, A; Furie, B.C.
J; Blol. Chem. 261, 13210-13215, 1986
A; Reference number: A37551; MUID:87008532; PMID:3759958
A; Contents: annotation; activation cleavages
R; MacGillivray, R.T.; Irwin, D.M.; Gilnto, E.R.; Stone, J.C.
Ann. N. X. Acad. Sci. 485, 73-79, 1986
                                                     A; Molecule type: mRNA
A; Residues: 384-618, E' <BAN>
A; Cross-references: GBs: M8139 at the companie of the c
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F;28.88/Domain: gla domain homology <GLA>
F;48.618/Domain: Gla domain homology <GLA>
F;44.618/Domain: gla domain b #status predicted <MAT>
F;44.618/Domain: kringle homology <KR2>
F;315-293/Domain: kringle homology <KR2>
F;50.51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat F;61.66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-54 F;403,459,565/Active site: His, Asp, Ser #status predicted
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A;Reaidues: 8-163,'N',165-622 <DE2>
A;Cross-references: GB:V00595; GB:J00307; NID:g37128; PIDN:CAA23842.1; PID:g1335344
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A; Residues: 188-311 <DE3>
R; Walz, D.A.; Hewett-Emmett, D.; Seegers, W.H.
Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
A; Reference number: A37549; MUID:77193964; PMID:266717
A; Accession: A37549
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A;Status: preliminary
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A; Residues: 1-618 <-DEG>
A; Residues: 1-618 <-DEG>
A; Residues: 1-618 <-DEG>
A; Cross-references: GS: X52308; NID: 953813; PIDN: CAA36548.1; PID: 953814
A; Cross-references: Strain CS'BL/6
A; Note: the data were obtained from females resulting from the cross of M. domesticus an A; Note: the data were obtained from females resulting from the cross of M. domesticus an A; Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 98, 2779-2783, 1992
A; Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq A; Reference number: A42696; MUID: 92212913; PMID: 1557383
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25-43/Domain: propeptide *status predicted <PRO>
28-88/Domain: gla domain homology <GLA>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 03-May-2002
C;Accession: A35827; A42696; S12081
R;Degen, S.U.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pai, J.A.
DNA Cell Biol. 9, 487-498, 1990
A;Title: Characterization of the cDNA coding for mouse prothrombin and localization of the A;Reference number: A35827; MUID:91025551; PMID:2222810
A;Status: preliminary
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A; Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute
B; Banfield, D; X; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A; Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A; Reference number: A42696; MUID:92212913; PMID:1557383
A; Accession: B42696
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A;Cross-references: EMBL:X52835; NID:956969; PIDN:CAA37017.1; PID:956970
B;Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.
Endocrinology 126, 167-175, 1990
A;Title: Profuncional levels are increased in the estrogen-treated immature rat uterus. A;Reference number: A60576; MUID:90091942; PMID:2293980
A;Accession: A60576
                                         C; Species: Rattus norvegicus (Norwers)
C; Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 03-May-2002
C; Accession: S10511; A60576; B42696
R; Dibanich, M; Monard, D.
Nucleic Acids Res. 18, 4251, 1990
A; Title: cDNA sequence of rat prothrombin.
A; Reference number: S10511; MUD:90332426; PMID:2377469
A; Accession: S10511
A; Molecule type: mRNA
A; Residues: 1-617 <DIH>
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Molecule type: mRNA
Residues: 383-617, E' <BAN>
Cross references: GB:M81397
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A; Reference number: A37552
A; Accession: A37552
A; Note: the evidence for 231-Ser is strong sites were determined
A; Redidues: 44-287, N', 289-352, 'E', 354,'Q', 356-548,'ND', 551-599,'N', 601-625 <AAG>
A; Note: the evidence for 231-Ser is strong sites were determined
A; Note: the evidence for 231-Ser is strong sites were determined
A; Note: the evidence for 231-Ser is strong sites were determined
A; Park, C. H.; Tulinsky, A.
Biochemistry 25, 3977-3982, 1986
A; Title: Tiree-dimensional structure of the kringle sequence: structure of prothrombi
A; Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms
B; Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms
B; Tirvin, D. M.; Aherin, K. G; Pearson, G.D.; MacGillivray, R.T.A.
B; A; Title: Characterization of the bovine prothrombin gene.
A; Reference number: A37554; MUID: 86077733; PMID: 3000440
A; Contents: annotation; gene structure
B; MacGillivray, R.T.; Degen, S.J.; Chandra, T.; Woo, S.L.; Davie, E.W.
A; Chandra, Cloining and annalysis of a cDNA coding for bovine prothrombin.
A; Reference number: I46045; MUID: 81054926; PMID: 6254059
A; Accession: I46045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Comment: Thrombin can cleave the amino-terminal activation peptide 1 from prothromb c;Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carb cicomment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carb interaction with the negatively charged phospholiphid membrane surface.
C;Comment: The prothrombin precursor is synthesized in the liver.
C;Superfamily: thrombin, Gla domain homology; kringle homology; trypsin homology C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; duplication; gl;F;1-24/Domain: signal sequence #status predicted <PRO>
F;28-84/Domain: ada domain homology (Glab)
F;38-84/Domain: activation peptide 1 #status experimental <FRI>F;109-187/Domain: kringle homology <RRI>F;210-292/Domain: kringle homology <RR2>
F;214-292/Domain: kringle homology <RR2>
F;318-36/Product: thrombin light chain #status experimental <ACH>
F;367-615/Domain: trypsin homology <TRY>
F;367-616/Domain: trypsin homology <TRY>
F;367-616/Fyromain: trypsin homology <TRY>
F;367-616/Fyrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 466-599, NV, 601-625 < MA2>
A; Residues: 466-599, NV, 601-625 < MA2>
A; Cross-references: EMBL: VO0135; NID: 9772; PIDN: CAA23451.1; PID: 9808945
B; Peller, G.; Karlstroem, A.R.; Berg, L.
Eur. J. Blochem. 227, 102-107, 1995
A; Title: Identification of the proteolytic thrombin fragments formed after cleavage w A; Reference number: 867518; MUID: 95154277; PMID: 7851376
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F;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;50,51,58,60,109-187,130-170,158-182,214-292,235-275,263-287,339-485,394-410,539-55
F;120,144,419/Minding site: carbohydrate (Asn) (covalent) #status experimental
F;409,465,571/Active site: His, Asp, Ser #status experimental
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 318-325;333-338,'X',340;367-374;481-484,'X',486-488;515-522 <PEJ>
C;Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fi
C;Comment: Prothrombin is activated on the surface of a phospholipid membrane that bi
tivation peptide and cleaves the remaining part into light and heavy chains. The acti
             Prothrombin and Related Coagulation Factors, Hemker, H.C.;
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S00845
Phopsin (EC 3.4.21..) - human
C;Species: Homo sapiens (man)
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Matches 10; Conserv
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A introns: 27/1; 80/3; 89/1; 106/1; 41/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552

C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C; Reywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli
C; Reywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli
E; 124/Domain: signal sequence #status predicted <PRO>
F; 25-43/Domain: propeptide #status predicted <PRO>
F; 28 87/Domain: propeptide #status experimental <PAT>
F; 44-32/Domain: activation peptide #status experimental <ART>
F; 108-186/Domain: kringle homology <RRI>
F; 213-291/Domain: kringle homology <RRI>
                                                                                                                                                                                                                      A Molecule type: mRNA

C MRNA

C Molecule type: mRNA

C MRNA
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F;364-622/Product: thrombin heavy chain #status experimental <RCH>
F;364-622/Product: thrombin heavy chain #status experimental <RCH>
F;364-623/Domain: trypsin homology <TRY>
F;364-65,30-62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status F;60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status F;121,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;336-550,564-594/Disulfide bonds: #status predicted
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R;MacGillivray, R.T.A.; Davie, E.W.
Biochemistry 23, 1626-1634, 1984
A;Title: Characterization of bovine prothrombin mRNA and its translation product.
A;Reference number: A00915; MUID:84203525; PMID:6326805
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C; Date: 24-Apr-1984 #sequence_revision 14-Jul-1994 #text_change 18-Jun-1999
C; Date: 24-Apr-1984 #sequence_revision 14-Jul-1994 #text_change 18-Jun-1999
C; Accession: S02537; A00915; A37552; 146045; S67518
R; Irwin, D.M.; Robertson, R.A.; MacGillivray, R.T.A.
J. Mol. Biol. 200, 31-45, 1988
A; Title: Structure and evolution of the bovine prothrombin gene.
A; Reference number: S02537; MuID:88245190; PMID:3379642
A; Accession: S02537
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Title: Recombinant genetic approaches to functional mapping of thrombin. Reference number: 151952; MUID:87182874; PMID:3471151
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5,462/Active site: His, Asp #status predicted
5/Binding site: carbohydrate (Asn) (covalent) #status experimental
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R;Magnusson, S.; Sottrup-Jensen, L.; Petersen, T.E.; Claeys,
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                                                                                                                                                                         Status: translated from GB/EMBL/DDBJ
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A: Residues: 1-230, 'H', 232-625 <MAC>
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Best Local Similarity
Matches 10; Conserv
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Gaps

Gaps

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Length 225;

DB 2; 0.095

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Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vita Superfamily: coaqulation factor X; EGF homology; Gla domain homology; trypsin homol Keywords: anticoaqulant; beta-hydroxyaspartic acid; blood coaqulation; calcium bind 1-29/Domain: signal sequence (fragment) *status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Comment: Protein C is synthesized in the liver as a single chain precursor, which i bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this rea C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with s cognition of the thrombin-thrombomodulin complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: protein | Residues: 197-454, PV | CSTES | Residues: 197-454, PV | CSTES | Residues: 197-454, PV | CSTES | Residues: 197-455, PW | CSTES | Residues: 197-4553, 1983 | Residues: 288, 5548-5553, 1983 | Residues: 288, 5548-5553, 1983 | Residues: 288, FSTES | Residu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 258, 5554-5560, 1983
Fitle: Structural changes required for activation of protein C are induced by Ca2+; Reference number: A37542; MUD:83213514; PMID:6406503
COntents: annotation; activation; calcium binding
Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nylternate names: autoprothrombin IIA; plasma protein C
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C;Accession: A26250; A18385; A8386; A00928
R;Long, G.L.; Balagaje, R.M.; MacGilliuvray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. Bi, 5653-5656, 1984
A;Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A;Reference number: A26250; MUID:85014826; PMID:6091100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-456 < LON>
B; Fernlund, P.; Stenflo, J.
J. Biol. Chem. 257, 12170-12179, 1982
A; Title: Amino and sequence of the light chain of bowine protein C.
A; Reference number: A18385; MUID: 83007325; PMID: 6896876
A; Accession: A18385
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A; Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C. A; Reference number: A19316; MUID:83169769; PMID:6572939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Contents: annotation; revision to residue 110

Stenflo, J.; Fernlund, P.
Balol. (Chem. 257, 12180-12190, 1982

Filtle: Amino acid sequence of the heavy chain of bovine protein C.

Reference number: A18386; MUID:83007326; PMID:6896877
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;30-39/Domain: propeptide #status predicted <PRO>
;40-194/Product: protein C light chain #status experimental <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (activated) (EC 3.4.21.69) precursor - bovine (fragment)
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F:197-456/Product: protein C heavy chain #status experimental <1
F:197-210/Domain: activation peptide #status experimental <APT>
                                                                                                                                 Score 53; DB;
Pred. No. 0.099
0; Mismatches
C, Superfamily: trypsin; trypsin homology C, Keywords: hydrolase; serine proteinase
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                                                                                                                                 Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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Residues: 40-194 <FER>
Note: 82-Lys was also found
                                                                                                                                                                                                                                                                                                                                                                                174 CEGDSGGPLV 183
                                                                                                                                                                                                                                                                                                                           1 CEGDSGGPFV 10
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submitted to the EMBL Data Library, March 1998
A;Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from X6
A;Reference number: 220829
                                                                                          R.Leytus, S.P.; Loeb, K.R.; Hagen, F.S.; Kurachi, K.; Davie, E.W.
Biochemistry 27, 1067-1074, 1988
A;Title: A novel trypsin-like serine protease (hepsin) with a putative transmembrane dom A;Reference number: $00845; MUID:88209431; PMID:2835076
A;Accession: $00845
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A; Cross_references: EMBL:U81290; NID:g2981640; PID:g2981641; PIDN:AAC24717.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Jaccession: S4356
R; Dihanich, M.; Spiess, M.
Biochim. Biophys. Acta 1218, 225-228, 1994
A; Title: A novel serine proteinase-like sequence from human brain.
A; Reference number: S45356; MUID: 94289486; PMID: 8018728
A; Accession: S45356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Xenopus laevis (African clawed frog)
Date: 22-oct-1999 #sequence_revision 22-oct-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X75363; NID:g407137; PIDN:CAA53145.1; PID:g940540
A;Experimental source: Alzhelmer's disease patient brain cortex
              31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
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                                                                                                                                                                                                                                                                                                                                A; MOlecule type: mRNA
A; Residues: 1-417 <LEY>
A; Cross-references: EMBL:X07732; NID:932063; PIDN:CAA30558.1; PID:932064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane protein
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F:188-204,291-359,322-338,349-381/Disulfide bonds: #status predicted
F:203,257,353/Active site: His, Asp, Ser #status predicted
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Pred. No. 0.18;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.9%; Score 56; DB 1; Length 417; 90.0%; Pred. No. 0.052; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:HPN; TWPRSS1; hepsin
A;Cross-references: GDB:135685; OMIM:142440
A;Map position: 19q11-19q13.2
C;Superfamily: hepsin: trypsin homology
C;Keywords: hydrolase; liver; serine proteinase; trans
F;23-45/Domain: transmembrane #status predicted <TMN>
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Best Local Similarity 90.0%;
Matches 9; Conservative
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A; Residues: 1-225 <DIH>
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Matches 9; Conserv
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F;211-440/Domain: trypsin homology <TRY>
F;45,46,53,55,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #state F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental F;110/modified site: erythro-beta-hydroxyaspartic acid (Asp) #status preprimental F;119-128,137-148,144-157,159-172,180-318,237-253,368-382,39421/pisulfide bonds: #state F;136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted F;252,298,397/Active site: His, Asp, Ser #status predicted F;366/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Gaps ö Query Match

89.8%; Score 53; DB 1; Length 456;
Best Local Similarity 90.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 1; Indels

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Search completed: May 12, 2003, 15:39:40 Job time : 12.4 secs

Sequence 4, App Sequence 2, App Sequence 163, Sequence 163, Sequence 163, Sequence 19, App Sequence 19, App Sequence 13, App Sequence 14, App Sequence 16, Sequence 16,

Sequence 4 Sequence 5 Sequence 6

Sequence Sequence Sequence

Sequence 247, Sequence 19

OM protein

Run on:

Searched:

Database

Result

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APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Simmons, David J.
APPLICANT: Simmons, David J.
APPLICANT: Samons, David J.
APPLICANT: Redin, William R.
TILLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROWBIN
TILLE OF INVENTION: PEPTIDE DERIVATIVES
FILE REFERENCE: 3033.1002-004
CURRENT PILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR APPLICATION NUMBER: 00/-19
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR FILING DATE: 2000-07-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: fragment of human prothrombin US-10-050-692-1
                                                                                                                                                                                                                         US-09-919-048-163
                                                                                                                                                                                                                                                                                                                                                                 US-09-946-633-19
US-09-826-290-247
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10050688; Publication No. US20020198154A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/10050692 Publication No. US20020182205A1 GENERAL INFORMATION:
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                                                                                                                                                                              Query Match
Best Local Similarity
Matches 10; Conserv
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US-10-050-688-1
TYPE: PRT
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                                                                                                       May 12, 2003, 15:38:52; Search time 19.4 Seconds (without alignments) 47.436 Million cell updates/sec
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Sequence 5, M
Sequence 6, M
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Sequence 5, Sequence 5, Sequence 5, Sequence 5, Sequence 5, Sequence 6, Sequence 45, Sequence 41, Sequence 41,
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Sequence 2,
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Sequence 3,
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/cgn2_6/ptodata/1/pubpaa/PS06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PS06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
               GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-050-611-3
US-10-050-611-4
US-10-050-688-5
US-10-050-688-6
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US-09-909-122-5
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US-09-909-122-1
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                                                                                                                                                                                                                                                                            349150 seqs, 92025710 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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59
1 CEGDSGGPFV 10
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Publication No. US20020187933A1

GENERAL INFORMATION:

TILLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED

TILLE OF INVENTION: PEPTIDES

FILE REFERENCE: 3033.1000-008

CURRENT APPLICATION NUMBER: US/10/050,611

CURRENT PILING DATE: 2002-01-16

PRIOR FILING DATE: 2001-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12
                       APPLICANT: Yang, Jinping
APPLICANT: Redin, William R.
TITLE OF INVENTION: Stimulation Of Bone Growth With Thrombin
TITLE OF INVENTION: Peptide Derivatives
FILE REFERENCE: 3033.1002-001
                                                                                                                                                                                                                                                                                                                                                                                        Length 10;
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Patent No. US20020061852A1
GENERAL INFORMATION:
APPLICANT: Carney, Darrell
TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59; DB 9;
Pred. No. 0.0024;
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                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/219,300 PRIOR FILING DATE: 2000-07-19 NUMBER OF SEQ ID NOS: 5 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 10
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                    CURRENT APPLICATION NUMBER: US/09/909,122 CURRENT FILING DATE: 2001-07-19
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 10; Conservative
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US-09-904-090-2
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SEQ ID NO 2
LENGTH: 12
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APPLICANT
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APPLICANT: Stiernberg, Janet
APPLICANT: Bergmann, John
TITLE OF INVENTION: STIMULATION OF CARTILLAGE GROWTH WITH
TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
TITLE OF INVENTION: RECEPTOR
FILE REPRENCE: 3033.1003-004
CURRENT APPLICATION NUMBER: US/10/050,688
CURRENT FILING DATE: 2002-01-16
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100.0%; Pred. No. 0.002;
:lve 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.002;
tive 0; Mismatches 0;
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CTHER INFORMATION: peptide fragment of thrombin
US-10-050-688-1
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                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/219,800
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 10
                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/909,348 PRIOR FILING DATE: 2001-07-19
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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US-09-909-122-1
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OTHER INFORMATION: c:terminal amidated fragment of human thrombin
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TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
TITLE OF INVENTION: PEPTIDES
FILE REPERENCE: 3033.1000-008
CURRENT APPLICATION NUMBER: 05/10/50,611
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/904,090
PRIOR FILING DATE: 5000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
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TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED ITTLE OF INVENTION: PEPTIDES
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Pred. No. 0.0044;
; Mismatches 0;
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; OTHER INFORMATION: valine is amidated as CONH2
US-10-050-611-4
                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: human fragment of thrombin US-10-050-611-3
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                                          FILE REFERENCE: 3033.1000-008
CURRENT APPLICATION NUMBER: US/10/050,611
CURRENT APPLICATION NUMBER: 09/904,090
PRIOR APPLICATION NUMBER: 09/904,090
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 23
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10050611 Publication No. US20020187933A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Matches 10; Conservative
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APPLICANT: Crowther, Roger S.
APPLICANT: Stamons, David J.
APPLICANT: Stamons, David J.
APPLICANT: Stamons, David J.
APPLICANT: Redin, William R.
APPLICANT: Redin, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN TITLE OF INVENTION: STIMULATION OF BORIZES.
FILE REFERENCE: 3033.1002-004
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR APPLICATION NUMBER: 2000-07-19
SEQ ID NOS: 6
SEQ ID NO 6
IENGTH: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Polypeptide, fragment of thrombin US-09-904-090-2
                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 100.0%; Score 59; DB 10; Best Local Similarity 100.0%; Pred. No. 0.0024; Matches 10; Conservative 0; Mismatches 0;
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; LOCATION: (23)...(23)
; OTHER INFORMATION: Valine is amidated as ConH2
US-10-050-692-6
  FILE REFERENCE: 3033.1000-001
CURRENT APPLICATION NUMBER: US/09/904,090
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US 60/217,583
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 12
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Publication No. US20020182205A1
GENERAL INFORMATION:
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Matches 10; Conserv
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                                 TITLE OF INVENTION: STAULATION OF CARTILAGE GROWTH WITH
TITLE OF INVENTION: STAULATION OF THE NON-PROTECLYTICALLY ACTIVATED THROMBIN
TITLE OF INVENTION: RECEPTOR
FILE REPERENCE: 3033.1003-004
CURRENT APPLICATION NUMBER: US/10/050,688
CURRENT PILING DATE: 2002-01-16
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Carney, Darrell H.
APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Stiernberg, Janet
APPLICANT: Stiernberg, Janet
APPLICANT: Stiernberg, Janet
APPLICANT: BERGMANN, JOHN
TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
TITLE OF INVENTION: RECEPTOR
FILE REFERENCE: 3033.1003-004
CURRENT APPLICATION NUMBER: US/10/050,688
PRIOR APPLICATION NUMBER: 09/909,348
PRIOR PLILING DATE: 2001-07-119
PRIOR FILING DATE: 2001-07-119
PRIOR FILING DATE: 2000-07-20
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100.0%; Pred. No. 0.0044;
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: peptide fragment of thrombin US-10-050-688-5
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 23
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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; OTHER INFORMATION: CONH2
US-10-050-688-6
Stiernberg,
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Patent No. US20020032314A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARET DARRELL H.
APPLICANT: RAMARRISHNAN, SHYAM
TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS
FILE REFERENCE: CHEP:00.
CURRENT APPLICATION NUMBER: US/09/777,328
CURRENT FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
TITLE OF INVENTION: PEPFIDES
FILE REPERENCE: 3033.1000-001
CURRENT APPLICATION NUMBER: US/09/904,090
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US 60/217,583
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PARTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 23
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- O'THER INFORMATION: Polypeptide, fragment of thrombin US-09-904-090-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
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                                                                                                                                                                     PRIOR APPLICATION NUMBER: 2001-02-05
PRIOR APPLICATION NUMBER: 08/330,594
PRIOR FILING DATE: 1994-10-28
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
LENGTH: 23
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Sequence 8, Application US/09777328 Patent No. US20020032314A1
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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APPLICANT: Carney, Darrell H.
APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Stlernberg, Janet
APPLICANT: Stlernberg, Janet
APPLICANT: Stlernberg, Janet
APPLICANT: Bergmann, John
TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re
FILE REFERENCE: 3033.1003-001
CURRENT APPLICATION NUMBER: US/09/909,348
CURRENT FILING DATE: 2001.07-19
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APPLICANT: Yang, Jinping
APPLICANT: Redin, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROWBIN
TITLE OF INVENTION: PEPPINE DERIVATIVES
FILE REFERENCE: 3033-1002-004
CURRENT APPLICATION NUMBER: US/10/050,692
CURRENT APPLICATION NUMBER: US/10/050,692
PRIOR APPLICATION NUMBER: 09/909,122
PRIOR PILING DATE: 2001-07-19
FRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 25
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100.0%; Score 59; DB 10;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 0.0048;
tive 0; Mismatches 0;
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COTHER INFORMATION: fragment of human prothrombin
US-10-050-692-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-909-348-5; Sequence 5, Application US/09909348; Patent No. US20020042373A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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US-09-909-348-1 59 1 CEGDSGGPFV 10 Perfect score: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

908470 seqs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981. A_Geneseq_101002:* Database :

IDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT IDS2/gcgdata/geneseg/genesegp-emb /SIDS2 /SIDS2 /SIDS2

IDS2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score		% Query Match Length DB ID	DB	OI	Description	:
7	59	100.0	10	23	AAE20155	Serine esterase co	
7	59	100.0	10	23	AAU78372	Serine esterase co	
m	59	100.0	12	23	AAM50857	Serine esterase co	
4	59	100.0	23	20	AAW83414	Cell growth/adhesi	
ហ	59	100.0	23	21	AAB12893	Nerve tissue regen	
9	59	100.0	23	22	AAB70363	Human thrombin rec	
7	59	100.0	23	23	AAE22563	Human thrombin hig	
80	59	100.0	23	23	AAE20159	Human thrombin pep	
б	59	100.0	23	23	AAU78376	Thrombin peptide d	
10	59	100.0	23	23	AAM50858	Thrombin-derived p	

Bovine zeta 2 preth Human thrombin Asn Wild-type thrombin K5 Mutant thrombin E2 Mutant thrombin E2 Mutant thrombin E2 Mutant thrombin E2 Mutant thrombin E2 Mutant thrombin E2 Mutant thrombin R2 Mutant thrombin R2 Mutant thrombin R2 Mutant thrombin R2 Mutant thrombin N5 Mutant thrombin N5 Mutant thrombin W5 Mutant thrombin W5 Mutant thrombin W5 Mutant thrombin W6 Mutant thrombin N6 Mutant thrombin W6 Mutant thrombin W6 Mutant thrombin W6 Mutant thrombin W6 Mutant thrombin W6 Mutant thrombin W6 Mutan prethrombin CD4/Thrombin Human CD4/thrombin Human prothrombin Human prothrombin Human prothrombin Human prothrombin Human prothrombin	
AAW99113 AAAW99115 AAAW99115 AAAW1775 AAR74777 AAR74777 AAR74778 AAR76033 AAR76034 AAR76035 AAR76036 AAR76039	AARSO 741 AAR96216 AAR90377 AAW11543 AAY49566 AAU68931
	117 117 22 22
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ALIGNMENTS

AAE20155 standard; peptide; 10 AA. RESULT 1

18-JUN-2002 (first entry) AAE20155;

Serine esterase conserved peptide #1.

Cartilage growth; cartilage repair; arthritic joint; traumatic injury; non-proteolytically activated thrombin receptor; NPAR; chondrocyte; therapy; implantation; serine esterase conserved peptide.

Unidentified.

WO200207748-A2.

31-JAN-2002.

19-JUL-2001; 2001WO-US22668.

20-JUL-2000; 2000US-219800P

(TEXA) UNIV TEXAS SYSTEM.

Bergmann J; Carney DH, Crowther RS, Stiernberg J,

WPI; 2002-268953/31.

Stimulating growth and repair of cartilage, useful for treating e.g. arthritis, by local administration of an agonist of non-proteclytically activated thrombin receptor

Length 10;

DB 23;

Score 59;

10 AA;

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Sequence
                       Query Match
                                                                                                                                                   AAM50857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a method of stimulating bone growth at a site in a subject in need of osteoinduction. The method involves administering an agonist to stimulate bone growth at a site in a subject (e.g. a farm animal, companion animal or laboratory animal), in need of osteoinduction, such as the site in need of a bone graft in a subject, a segmental bone gap, a bone void or a non-union fracture. This sequence represents a serine esterase conserved sequence obtained from a serine esterase that can stimulate or activate the non-proteolytically
                                                                                                                                                                                                                                                                                                                                                                                                                                  serine esterase; osteopathic; thrombin; receptor; agonist;
bone growth stimulation; osteoinduction; farm animal; companion animal;
laboratory animal; bone graft; segmental bone gap; bone void;
non-union fracture.
                               The invention relates to a method of stimulating growth and repair of cartilage. The method involves administering to the site, an agonist of non-proteolytically activated thrombin receptor (NRAR). The method is used in human or veterinary medicine for the treatment of arthritic joints and damage/loss of cartilage caused by traumatic injury. Also chondrocytes may be cultured in presence of NPAR agonist to provide cells for implantation at sites requiring growth/repair of cartilage. The present sequence is serine esterase conserved peptide. This sequence is present in the thrombin peptide derivatives which serve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stimulating bone growth at a site in a subject in need of osteoliduction, such as a site of bone graft, segmental bone gap, bone void or non-union structure, by administering agonist of activated thrombin receptor
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100.0%; Pred. No. 0.081;
ive 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                      Serine esterase conserved sequence #1.
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                                                                                                                                                                                                                                                                                                                                           AAU78372 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 21; 27pp; English.
           Claim 7; Page 24; 28pp; English.
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Best Local Similarity 100.
Matches 10, Conservative
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                                                                                                                                                                                                                                                    as a NPAR agonist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                            Sequence
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AAU78372
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present peptide comprises a thrombin-derived serine esterase conserved sequence that is used in a claimed method for promoting cardiac tissue repair. The method involves administering an angiogenic thrombin-derived peptide, especially a thrombin receptor binding domain comprising the 4-amino acid peptide given in AAN50856 together with the serine esterase conserved sequence, or preferably the peptide given in AAN50858, which includes both these peptide sequences. The thrombin-derived peptide is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            administered during or following cardiac surgery by injection into cardiac tissue, and may be formulated as a sustained release formulation. It is used in claimed methods of stimulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vascular occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine esterase conserved sequence used in cardiac tissue repair.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine esterase; thrombin; revascularisation; vascular occlus
tissue repair; vulnerary; vasotropic; cardiant; anglogenesis;
restenosis; therapy; enzyme; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         revascularisation, stimulating vascular endothelial cell proliferation, inhibiting vascular occlusion, and inhibiting restenosis following balloon angioplasty, in which case the
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                                                  Mismatches.
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                                                                                                                                                                                                                                                                                             AAM50857 standard; Peptide; 12 AA.
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100.0%;
100.0%;
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                                                Conservative
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Best Local Similarity
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                      Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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RESULT 4 AAW83414 Synthetic

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contains a peptide immobilised to a base which consists of a contains a peptide immobilised to a base which consists of a bylysaccharide gel such as alginic acid. Sequences AABI2886-B12899 represent examples of the peptides used in the nerve regeneration material. The peptide containing material causes nerve cell repoil fersation and also causes axonal extension. The material can be used for the treatment of central or peripheral nervous system disorders, spinal disorders, head injury or cerebrovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New synthetic neutrophil cell chemotactic peptides, useful for generating antibodies for modulating neutrophil chemotaxis in immune response and wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neutrophil cell chemotactic; wound healing; inflammation; vulnerary; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to a new nerve regenerative material which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human thrombin receptor binding domain peptide SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 59; DB 21
100.0%; Pred. No. 0.16;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Column 6; 15pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 5; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nerve regeneration material
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                                                                                                                        99JP-0227108
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                       (KURS ) KURARAY CO LID. (NISH/) NISHIMURA Y: (SUZU/) SUZUKI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-202003/20.
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-415772/36
                                                                                                                                                                                                                                                                                                                          (SUZU/) SUZUKI Y.
(TANI/) TANIHARA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CEGDSGGPFV 10
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JP2000143531-A.
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                                                                                                                               11-AUG-1999;
                                                                  23-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide or its salt as the active component. The peptide and its salt can be used for covering injuries, promoting adhesion of biotissues, bone reinforcing and nerve regeneration. The present sequence represents a specifically claimed peptide of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a material for medical treatment which comprises one or more peptides of the formula XADEGJIMProQY, or their salts, immobilised on a substrate: where X = H, CH3CO or CH3COLys;
A = Ser or Th; D = Ile, Val or Leu; B = Lys or Arg; G = Ile, Val or Leu; J = Gly or Ala; L = Ile, Val or Leu; M = Gly or Ala; D = Gly, Ala or Gly-Lys-Lys-Lys-Cly; T = OH or NH2. Also described is an agent for cell growth promotion and/or cell adhesion promotion containing the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Material for medical treatment comprises new peptide - used for covering injuries, promoting adhesion of bio-tissues, bone
                                                                                                                                                                                                                                                                                                                                                                  Cell growth; adhesion; promotion; medical treatment; injury; biotissue; bone reinforcement; nerve regeneration; HMP resin
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                                                                                                                                                                                                                                                                                                      Cell growth/adhesion promoting peptide #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reinforcing and nerve regeneration
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                                                                                                       AAW83414 standard; peptide; 23 AA.
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Synthetic

AAB12893;

Sequence

Matches

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Gaps

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Length, 23; Indels 23 AA;

Sequence

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neutrophil cell chemotactic agent. (I) has vulnerary and antiliflammatory activities. (I) is useful as a potent neutrophil cell chemotactic agent and for generating antibodies against the peptides, which are useful for modulating neutrophil recruitment to a wound site for enhancing or inhibiting inflammation and early effects of wound healing. Neutrophil response to (I) is specific, since monocytes and fibroblasts do not show any expression of the receptor to which (I) binds. The present sequence represents a human thrombin receptor bliding domain peptide which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel synthetic peptides and antibodies which are potent chemotactic agents for neutrophils. The peptides of the invention mimic the activity and role of the cleavage fragment of the proteolytically activated receptor for thrombin (PART). They are useful for stimulating or modulating neutrophil cell chemotactic migration or for generating an antibody. In particular, the peptides of the invention are useful for modulating neutrophil recruitment to a wound site for enhancing or inhibiting inflammation and early effects in wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            They are also useful for modulated neutrophil chemotaxis in immune response. The present sequence is high affinity receptor binding domain of human thrombin. This peptide is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New synthetic peptide neutrophil cell chemotactic agents, useful for stimulating or modulating neutrophil cell chemotactic migration, particularly for modulating neutrophil recruitment during immune
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; proteolytically activated receptor for thrombin; neutrophil; chemotactic agent; PART; inflammation; wound healing; chemotaxis; immune response; vulnerary; thrombin; receptor binding domain.
                        present invention describes a synthetic peptide (I) which is
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                                                                                                                                                                                                                                                                                  Length 23;
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100.0%; Pred. No. 0.16;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human thrombin high affinity receptor binding domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       response or in wound healing
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                                                                                                                                                                                                                                                                                                  Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of stimulating growth and repair of cartilage. The method involves administering to the site, an agonist of non-proteolytically activated thrombin receptor (NRRN). The method is used in human or veterinary medicine for the treatment of arthritic joints and damage/loss of cartilage caused by traumatic injury. Also chondrocytes may be cultured in presence of NRRR agonist to provide cells for implantation at sites requiring growth/repair of cartilage. The present sequence is human thrombin peptide derivative which serves
                                     Gaps
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                                                                                                                                                                                                                                                                                                                             Cartilage growth; cartilage repair; arthritic joint; traumatic inju:
non-proteolytically activated thrombin receptor; NPAR; chondrocyte;
therapy; implantation; thrombin peptide; human.
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 Length 23;
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   DB 23;
                  0.16;
                                    Mismatches
   Score 59;
Pred. No.
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                                                                                                                                                                                                                                                                                              Human thrombin peptide derivative #2.
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 100.0%;
100.0%;
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                                                                                                                                                                                                                                                              (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
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Query Match
Best Local Similarity
Matches 10; Conserv
                                                                    1 CEGDSGGPFV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200207748-A2.
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                            18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2002
                                                                                                                                                                                                                          AAE20159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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AAU78376
ID AAU7
XX
AC AAU7
                                                                                                                                                       RESULT 8
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Promoting cardiac tissue repair, stimulating revascularisation, stimulating vascular endothelial cell proliferation, and inhibiting vascular occlusion by using anglogenic thrombin derivative peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               that includes a thrombin receptor binding domain sequence (see als AAM50856) and a serine esterase conserved sequence (see also AAM50857). The peptide is used in a claimed method for promoting cardiac tissue repair. It is administered during or following cardiac surgery by injection into cardiac tissue, and may be formulated as a sustained release formulation. The thrombin cormulated as a sustained release formulation. The thrombin proliferation, stimulating vascular endothelial cell proliferation, inhibiting vascular endothelial cell restances formulating vascular endothelial cell proliferation, inhibiting vascular occlusion, and inhibiting restances for the process of the case it may be restanced to the case it may be called to the case of the case it may be called to the case of the case
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23; Length 23;
                                                                                      "serine esterase conserved sequence"
10..13 /note- "thrombin receptor binding domain" 12..23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59; DB 23
Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW99113 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 19; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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100.0%;
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97US-0048864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine zeta 2 prethrombin 2.
                                                                                                                                                                                                                         12-JUL-2001; 2001WO-US21944.
                                                                                                                                                                                                                                                                        12-JUL-2000; 2000US-217583P
                                                                                                                                                                                                                                                                                                                  (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coated onto the catheter.
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                                                                      12..23
/note=
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-179665/23.
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 AA;
                                                                                                                                       WO200204008-A2.
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06-JUN-1997;
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                                                                                                                                                                                    17-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                 Carney DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW99113;
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       Key
Peptide
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                                                                        Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a method of stimulating bone growth at a site in a subject in need of osteoinduction. The method involves administering an agonist to stimulate bone growth at a site in a subject (e.g. a farm animal, companion animal or laboratory animal), in need of osteoinduction, such as the site in need of a bone graft in a subject, a segmential bone gap, a bone vid or a non-union fracture. This sequence represents a thrombin peptide derivative obtained from a serine esterase that can stimulate or activate the non-proteolytically activated thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stimulating bone growth at a site in a subject in need of osteoinduction, such as a site of bone graft, segmental bone gap, bone void or non-union structure, by administering agonist of activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                Thrombin; osteopathic; receptor; agonist; bone growth stimulation; osteoinduction; farm animal; companion animal; laboratory animal; bone graft; segmental bone gap; bone void; non-union fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thrombin; revascularisation; vascular occlusion; tissue repair; vulnerary; vasotropic; cardiant; angiogenesis; restenosis; therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Redin WR;
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100.0%; Pred. No. 0.16;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simmons DJ,
                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM50858 standard; Peptide; 23 AA.
                                                                          Thrombin peptide derivative TP508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 22; 27pp; English
                                                                                                                                                                                                                                                                                                       /label- Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2000; 2000US-219300P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-2001; 2001WO-US22641
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Best Local Similarity 100...
                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crowther RS,
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                                                                                                                                                                                                                                                                                  Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                   WO200205836-A2
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                                   18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carney DH,
                                                                                                                                                                                                                  Synthetic.
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AAM50858
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Indels

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WPI; 1999-070237/06.
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AAW11545
ID AAW11:
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  FFFXGXGXGXGX
                                                                                                                                                      An exosite assay has been developed for inhibition of the catalytic cleavage of prothrombin (PTh) to thrombin (Th) by prothrombinase (I), at a site remote from the catalytic site of (I) comprises: (a) preparing a solution containing 0.05-20 mu M substrate (S), that includes a protease cleavage site and exosite-binding determinant; 0.05-200 mM factor Va; 0.50-50 micro M phospholipids (PL); test inhibitor (A) in buffer of pH (7-9, containing 1-10 mM calcium ions but no calcium-chelating agent; (b) initiating catalytic cleavage of (S) by adding an aliquot of factor Xa (to final concentration 0.05-200 mM) so that there is an excess of Va over Xa, forming a S/(I) complex; (c) withdrawing aliquots of the caection mixture, quenching them; and (d) assaying for concentration of Xa (less than the amount of Va), and reaction is started by adding S. Also described in the present invention are cinibitors (A') having IC50 less than 1 mu M identified by this assay. (A') are concentration as a new class of anticoagulants for treatment of cardiovascular disease, stroke and haematological disorders. The method is based on the finding that exosite interactions are critical for represent sequence concentrate specificity in catalytic formation of Th. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                 Exosite assay for agents that inhibit catalytic cleavage of prothrombin - at sites away from the active site of prothrombinase, also new inhibitors, potentially useful as anticoagulants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prothrombin; exosite assay; anticoagulant; blood clot; thrombin; cardiovascular disease; stroke; haematological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                represents bovine zeta 2 prethrombin 2
                                                                                                                                  Disclosure; Page 42-43; 61pp; English
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Best Local Similarity 100.0
Matches 10; Conservative
                                                          WPI; 1999-070237/06.
           (UYEM-) UNIV EMORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CEGDSGGPFV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 AA;
                                  Krishnaswamy S;
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06-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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An exosite assay has been developed for inhibition of the catalytic cleavage of prothrombin (PTh) to thrombin (Th) by prothrombinase (I), at a site remote from the catalytic site of (I) comprises: (a) preparing a colution containing 0.05-20 mu M substrate (S), that includes a protease cleavage site and exosite-binding determinant; 0.05-200 nM factor Va; 30-500 mCtor M phospholipids (PL); test inhibitor (A) in buffer of pH 7-9, containing 1-10 m Calcium ions but no cablcium-chelating agent; (C) initiating catalytic cleavage of (S) by adding an aliquot of factor Xa (to final concentration 0.05-200 nM) so that there is an excess of Va cover Xx, forming a S(I) complex; (C) withdrawing aliquots of the C reaction mixture, quenching them; and (d) assaying for concentration of Th. Alternatively, in the initial solution S is replaced by the same concentration of Xa (less than the amount of Va), and reaction is started by adding S. Also described in the present invention are inhibitors (A) having ICSO less than 1 mu M identified by this assay. (A) are potentially useful as a new class of anticoagulants for treatment of cardiovascular disease, stroke and haemacological disponders. The method is based on the finding that exosite interactions are critical for represents human zeta. 2 prethrombin 2.

The present sequence of the present sequence of the sequence of the sequence of the second sequence of the sequence of the sequence of the second sequence of the second sequence of the sequence of the sequence of the second second sequence of the sequence of
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Exosite assay for agents that inhibit catalytic cleavage of prothrombin - at sites away from the active site of prothrombinase, also new inhibitors, potentially useful as anticoagulants
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                                                                                                                                                                                                                                                                           Disclosure; Page 44-45; 61pp; English
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CEGDSGGPFV 10
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mutein; platelet aggregation; blood clotting;
decrease; hirudin; heparin; anti-thrombin III; AAW11545 standard; Protein; 259 AA. Human thrombin Asn99 mutant. (first entry) Prothrombin; mutant; reduce; coagulation; redu antagonist; D99N. Homo sapiens. Synthetic. 01-OCT-1997

/note= "Wild-type Asp residue has been replaced /label- thrombin_Asn99 Misc-difference 99 Location/Qualiflers WO9641868-A2

96WO-AT00105 95AT-0001006 12-JUN-1996; 13-JUN-1995; 27-DEC-1996.

(IMMO) IMMUNO AG.

Eibl J,

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The sequence reresents wild-type (reference) thrombin. Mutants of this sequence (AAR74776-80 and AAR76033-41) have at least 80% homology with thrombin, and are capable of protein-c activation without significant fibrinogen clotting activity, and vice versa clotting activity of less than 0.5 or greater than 2 compared to thrombin. The mutant thrombin sequences, produced in recombinant cell culture or by in vitro methods, and are used to treat thrombotic conditions, particularly during cardiac bypass surgery and in cases of septic shock.
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                                                                                                                                              Thrombin derivs with segregated pro- and anticoagulant activities useful for treating thrombotic disorders but also diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombin; oligonucleotide-directed mutagenesis; procoagulant; anticoagulant; protein engineering; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note- "Lys in wild-type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Arg in wild-type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR74776 standard; Protein; 295 AA.
                                                                                                                                                                                                                                                     Disclosure; Fig 1, 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsiang M;
                          Tstang M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant thrombin K52A, R233A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94WO-US13104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0258038
93US-0152657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                   treatment of tumours, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gibbs CS, Leung LLK,
                       Leung LLK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111111111
237 CEGDSGGPFV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GILE-) GILEAD SCI.
                                                                       WPI; 1995-194103/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CEGDSGGPFV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 AA;
                                                                                                 N-PSDB; AAQ92455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-1994;
12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9513385-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-1995.
                          Gibbs CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR74776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
õ
                                                                                                                                                                                                                                                   Prothrombin mutants having one or more changes in amino acid sequence compared with the natural protein and having 0.10% (preferably 0.0.25%) of the activity of the natural protein are claimed, provided that the changes in amino acid sequence do not affect the capacity of the mutants to bind to specific ligands and receptors. The mutants have greatly reduced clotting activity and are useful as antagonists of thrombin inhibitors such as hirudin, heparin and anti-thrombin III. The mutations may also result in changes to the in vivo half-life of prothrombin. The half-life may be reduced to less than 10 minutes or the mutant prothrombin may have an extended half-life of more than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   induction in the setul as an anticogulant and to inhibit side-
effects of anti-coagulant treatment. They are converted to inactive
thrombin and are able to compete with native, active thrombin for
binding to receptors. The present sequence represents the thrombin
mutant which is derived by trypsin cleavage of a specifically
claimed human prothrombin mutant in which asp at position 419 is
changed to Asn. The thrombin Asn99 mutant was found to have only
0.24% of the activity of wild-type thrombin on a chromogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Note: This sequence does not appear in the specification and has been produced by modifying the wild-type sequence of human prothrombin which appears in figure 1).
                                                                                                                            Prothrombin mutants with reduced clotting activity – useful as antagonists of thrombin inhibitors or for anticoagulant therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombin; oligonucleotide-directed mutagenesis; procoagulant; anticoagulant; protein engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 259;
                          Schlokat U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 59; DB 18;
100.0%; Pred. No. 1.2;
iive 0; Mismatches 0;
                             Mitterer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
37.295
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR74775 standard; Protein; 295 AA.
                          Falkner F, Fischer B,
                                                                                                                                                                                                        Example 3; Page -; 73pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0258038
93US-0152657
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                                                                            WPI; 1997-065455/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
tes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CEGDSGGPFV 10
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substrate.

Sequence Query Match

Best Loca Matches

14-NOV-1994; 10-JUN-1994; 12-NOV-1993;

W09513385-A 18-MAY-1995

Protein

Homo saptens

AAR74775;

RESULT 14

g ö

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Gaps

ö

Indels

useful for treating thrombotic disorders but also diagnosis, treatment of tumours, etc.

Claim 22; Page 63/3; 78pp; English.

The mutant thrombin sequence, generated by oligonucleotide-directed mutagenesis, has at least 80% homology with thrombin, and is seapable of protein-c activation without significant fibrinogen clotting activity, and vice versa. (specifically, it has a ratio of protein-C activity to fibrinogen clotting activity of less than 0.5 or greater than 2 compared to thrombin). The mutant thrombin is produced in recombinant cell culture or by in vitro methods, and is used to treat thrombotic conditions, particularly during cardiac bypass surgery and in cases of septic shock.

295 AA; Sequence

0; Gaps Query Match 100.0%; Score 59; DB 16; Length 295; Best Local Similarity 100.0%; Pred. No. 1.4; Matches 10; Conservative 0; Mismatches 0; Indels

· 1 CEGDSGGPFV 10 ð

Search completed: May 12, 2003, 15:36:02 Job time: 29.6 secs

OM protein

Run on:

Sequence:

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Q9dfdl oncorhynchu
Q91vq8 mus musculu
O45045 scirpophaga
Q924u6 mus musculu
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018448 helicoverpa
Q9ylk4 anopheles g
Q9dc82 mus musculu
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homo sapien
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drosophila
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boltenia vi
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                                                                                                                                                                                               botryllus s
Q9ttrO canis famil
Q90wd8 bufo japon
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drosophila
                                 O9vsu2 drosophila
O9uli2 drosophila
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                                                                                                         drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Banffeld D.K., McGillivray R.T.A.;
"Partial characterization of vertebrate prothrombin cDNAs:
Amplification and sequence analysis of the B chain of thrombin from
nine different species.",
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
EMBL. M81399; AAA48514.1; -.
HSSP: PO0(34; ZHNT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acipenser transmontanus (White sturgeon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
                                                                                                                                                                                                                                                                                                                                            09cq78
                                                                                                                                                                                             027458
017800
09vwd8
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09vzt0
09vh83
                                                                                                                                                                                                                                                                                                                                                               Q9nr68
                                                                                    Q9v513
Q8sy35
                                                                                                                                            0960g6
09nb78
                                                                       Q9u113
                                                                                                                          09b119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.
UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MERUPS; SUL.41,
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN.
PROSITE; PS00135; TRYPSIN_ER; 1.
Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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09VH83
09GTK6
09TV90
09CQ78
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Q9DC82
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                                                                                                                                                                                                              017800
09VWD8
09BPQ4
                                                                                                                                            990960
                                                                                                                                                             09NB78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-LIVER;
MEDLINE-92212913; PubMed-1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26846 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20, Thrombin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                       1462
1557
1674
2382
2409
187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; S01.217;
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NON_TER
SEQUENCE
   Acipenser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THROMBIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        090244
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Q90244
   SOLITA DE LA PERSONA DE LA PER
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09bk47 luidia foli
09cv97 mus musculu
091674 xenopus lae
09v514 drosophila
076498 diaprepes a
09670 homo sapien
045029 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             090387 cynops pyrr
091218 oncorhynchu
090504 eptatretus
091001 gallus gall
09ptw7 struthio ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        090244 acipenser t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          © Q91004 gecko gecko
Q90387 cynops pyrr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                           May 12, 2003, 15:32:37; Search time 22.6 Seconds (without alignments) 91:171 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                  671580
                    GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                 Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Q90504
Q91001
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Q9BK47
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Gapop 10.0 , Gapext 0.5
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p_unclassified:*
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sp_bacteriap:*
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seq length: 200000000
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sp_bacteria:*
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59
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Perfect score:
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Minimum DB s Maximum DB s

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Gaps
                                                    Banfield D.K., MacGillivray R.T.A.;
"Partial characterization of vertebrate prothrombin cDNAs:
Amplification and sequence analysis of the B chain of thrombin from
nine different species."
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-!- SIMILARIY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
EMBL; M81392, AAA43309.1; -.
HSSP; P00734; LB7X.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea; Salamandridae, Cynops
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Partial characterization of vertebrate prothrombin cDNAs:
Amplification and sequence analysis of the B chain of thrombin from
nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE
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R InterPro; IPR001234; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
R SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_1.
ROSITE; PS00135; TRYPSIN_ERR; 1.
ROSITE; PS00135; TRYPSIN_ERR; 1.
RSDUENCE 235 AA; 26933 MW; 1122A5C09F6F7;
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
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SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HS; UN
PROSITE; PS00135; TRYPSIN_SER; I.
Hydrolase; Serine procease.
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EMBL; M81395; AAA49391.1; -.
HSSP; P00734; 1UVS.
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01-MAR-2002 (TrEMBLrel. 20,
Thrombin (Fragment).
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Best Local Similarity 100.
Matches 10; Conservative
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SEQUENCE
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Q90387
REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amplification and sequence analysis of the B chain of thrombin fronted different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
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Usukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gekko.
NCBI_TaxID=36310;
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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                        100.0%; Score 59; DB 13; Length 234; 100.0%; Pred. No. 0.0097;
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"Partial characterization of vertebrate prothrombin
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Last sequence update)
Last annotation update)
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Last sequence update)
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100.0%; Score 59; DB 6; Lv
100.0%; Pred. No. 0.0098;
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                                                                                   0; Mismatches
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
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Best Local Similarity 100.
Matches 10; Conservative
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THROMBIN.
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MEDLINE-94223694; PubMed-7513365;
Banfield D.K., Irwin D.M., Walz D.A., MacGillivray R.T.;
"Evolution of prothrombin: isolation and characterization of the cDNAs encoding chicken and hagfish prothrombin.";
J. Mol. Evol. 38:177-187(1994).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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"Partial characterization of vertebrate prothrombin cDNAs:
amplification and sequence analysis of the B chain of thrombin from
nine different species.";
       Banfield D.K., MacGillivray R.T.;
"Partial characterization of vertebrate prothrombin cDNAs: amplification and sequence analysis of the B chain of thrombin from inte different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
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R PROSITE; PSO0021; KRINGLE.1; 1.
R PROSITE; PS50070; KRINGLE.2; 1.
R PROSITE; PS50240; TRYPSIN.DOM; 1.
PROSITE; PS00134; TRYPSIN.HIS; UNKNOWN.1.
PROSITE; PS00135; TRYPSIN.BER; 1.
Hydrolase; Serine protease.
SEQUENCE 420 AA; 47888 ww.
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Interpro; IPR000001; Kringle.
Interpro; IPR001254; Ser_protease_Try.
Pfam; PF00051; Kringle; 1.
Pfam; PF00089; trypsin; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
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PRINTS; PRO0018; KRINGLE.
PRODON; PDO00035; KRINGLE.
SMART; SM000130; KR; 1.
SMART; SM00020; Tryp_SPc; 1.
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HSSP; P00734; 1UVS.
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091001;
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Q91001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
Q
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                     IN SECTION OF SECTION 
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                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Banfield D.K., MacGillivray R.T.A.; *Partial characterization of vertebrate prothrombin cDNAs: Amplification and sequence analysis of the B chain of thrombin from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eptatretus stoutii (Pacific hagfish).
Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
Myxinidae; Eptatretinae; Eptatretus.
NCBI_PaxID=7765;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
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Pred. No. 0.0099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 AA; 27396 MW; FOF43F9A3205BF38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
0.0098;
                                                                                                                                                                                                                                                                          239 AA
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InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
Pfan, FP600089; trypaln; 1.
SMART; SM00020; Tryp_SPC; 1.
PR0SITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_LSE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                  Pred. No. 0.
                                                                                                                                                                                                                                                                                                                         Created)
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TISSUE-LIVER; — MEDLINE-92212913; PubMed-1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rissue=Liver;
Medline=92212913; PubMed=1557383;
  100.08; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Sc
100.0%; Pr
tive 0;
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                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Serine protease.
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Matches 10; Conservative
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                                               Conservative
                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                      Thrombin (Fragment).
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                                                                                                                              177 CEGDSGGPFV 186
                  Best Local Similarity
Matches 10; Conserv
                                                                                              1 CEGDSGGPFV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                             THROMBIN.
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EMBL; AF252869; AAF91346.1; -. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                PRINTS; PR00722; CHYMOTRYPSIN PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                     PRINTS; PRO0018; KRINGLE.
ProDom; PD000395; Kringle; 2.
EMBL; AB028871; BAA89046.1;
HSSP; P00734: 117VS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     50070; KRINGLE 2
                                                                                                                                                                             Pfam; PF00594; gla; 1.
Pfam; PF00051; kringle; 2.
Pfam; PF00089; trypsin; 1.
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hes 10; Conservative
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550 CEGDSGGPFV 559
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                                                  MEROPS; S01
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                                                                                                                                                                                                                                                                                                                 ProDom; 1
SMART; SI
                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE:
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Q9NBC9
    SO WE HAVE THE PROPERTY OF THE
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                                                              Banfield D.K., Irwin D.M., Walz D.A., MacGillivray R.T.; "Evolution of prothrombin: isolation and characterization of the cDNAs encoding chicken and hagfish prothrombin."; Mol. Evol. 38:177-187(1994).
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . J. Biochem. Cell Biol. 32:1151-1159(2000).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
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Pred. No. 0.025;
; Mismatches 0; Indels (
                                                                                                                                                                                                                                       Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
EMBL; M81391; AAA21619.1; -- HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Serine protease.
SECHENCE 607 AA; 69110 MW; 002F3606EA36270F CRC64;
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Last annotation update)
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PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001254; Ser_protease_Try
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100020; Tryp_SPc; 1.
PS00011; GLU_CARBOXYLATION;
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                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002383; GLA_blood.
                                           MEDLINE-94223694; PubMed-7513365;
                                                                                                                                                                                                                                                                                                                                                                               Kringle.
Prothrombin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00051; Kringle; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
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ProDom; PD000395; Kringle; 2.
SMART; SM00069; GLA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00594; qla; 1
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                                                                                                                                                                                                                                                                                                            501.217
                                                                                                                                                                                                                    Banfield D.K.;
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                                                                                                                                                                                                      LISSUE-LIVER;
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                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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Gaps
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Pterrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
NCBI_TaxID=37546;
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Yan J., Cheng Q., Li C.B., Aksoy S.;
"Molecular characterization of two serine proteases expressed in gut
tissue of the African trypanosome vector, Glossina morsitans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insect Mol. Biol. 10:47-56(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69392 MW; 11B974B9AEE54EA2 CRC64;
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21, Last annotation update)
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SWART; SW00020; Tryp_SPc; 1.
PROSITE; PS00340; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequenc
01-UTV-2002 (TrEMBLrel. 21, Last annocat
Trypsin-like serine protease precursor.
Glossina morsitans morsitans
                                                                                                                                                                                                                                                                                                                                                                                                           SM00020; Tryp_SPc; 1.
5; PS00011; GLU_CARBOXYLATION; 1.
8; PS00021; KRINGLE_1; 2.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002383; GLA_blood.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser_protesse_Try.
InterPro; IPR000294; VitK_dep_GLA.
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InterPro; IPR001254; Ser_protease_Try
Pfam; PF00089; trypsin; 1.
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TEDLINE-21085660; PubMed-11217851;
STRAIN-C57BL/6J; TISSUE-KIDNEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 CQGDSGGPFV 443
                                                                                                                                                                                                                                                                                     MEROPS; S01.224; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
                                                                                                                                                                                                           Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         091674;
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                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                     Gene 262:73-80(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                               Vickery M.C.L., Vickery M.S., McClintock J.B., Amsler C.D.; "Utilization of a novel deuterostome model for the study of regeneration genetics: Molecular cloning of genes that are differentially expressed during early stages of larval sea star
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adult male kidney CDNA, RIKEN full-length enriched library,
clone:0610030A17, full insert sequence (Fragment).
                                                                                                                                                                                                                              Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
Asteroidea; Valvatacea; Paxillosida; Luidiidae; Luidia.
NCBI_TaxID=105861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 5; Length 267;
Pred. No. 0.038;
                                  Length 255;
 255 TRYPSIN-LIKE SERINE PROTEASE. 27565 MW; E914E31FB7DD6579 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Protease; Serine protease.
SEQUENCE 267 AA; 28761 MW; 88F61A061921860C CRC64;
                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Sea StAR regeneration-associated protease SRAP.
                                 94.9%; Score 56; DB 5; 90.0%; Pred. No. 0.036; 11ve 1; Mismatches
                                                                                                                                                       267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO072; CHYMOTRYPSIN.
PRINTS; PRO072; CHYMOTRYPSIN.
PROATT; SMO020; TRYP_SES; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_I.
PROSITE; PS00135; TRYPSIN_ER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
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01-JUN-2001 (TrEMBLrel, 17, Last seq
01-JUN-2002 (TrEMBLrel, 21, Last anno
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-21100442; PubMed-11179669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.98;
                       Ouery Match
Best Local Similarity 90.00
2009 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 90.0
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                                                                                                                                                       PRELIMINARY;
 28 2
255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 COGDSGGPFV 221
                                                                                       1 CEGDSGGPFV 10
                                                                            1 CEGDSGGPFV 10
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                       Luidia foliolata.
                                                                                                                                                                                                                                                                                                                                              regeneration.";
   CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                      Q9BK47;
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Matches
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Ra Arawaw T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Radawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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Radota K., Matsuda H.S., Nikaido I., Rochiwa H.,
Radota K., Matsudo Y., Nikaido I., Rochiwa H.,
Radota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
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Radusincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Rochon P., Marchionni I., Mashima J., Mazzarelli J., Mombeerts P.,
Rochon P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
Radota K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Radota K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Radota K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Radota K., Sabara K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Radota K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Radota K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Radota K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Radota K., Wang K.H., Wang K.H., Wang K.H., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 502;
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Last annotation update)
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translated as part of an unusual polyprotease."
Proc. Natl. Acad. Sci. U.S.A. 96:11253-11258(199),
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90.0%; Pred. No. 0.072;
ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1524 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS: PR00089; TYPPS10; 1.
PRINTS: PR00722; CHYMOTRYPSIN.
SWART; SW00202; SR; 1.
PROSTIE; PS00098; THIOLASE_1; UNKNOWN_1.
PROSTIE; PS00098; TRYPSIN_DOM; 1.
PROSTIE; PS00135; TRYPSIN_DOM; 1.
HYDROLASE; Scrine Protesse.
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InterPro; IPR001314; Chymotrypsin:
InterPro; IPR001254; Ser_protease_Try
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-NOV-1996 (TrEMBLrel. 01, Created)
1-NOV-1998 (TrEMBLrel. 08, Last seq.
1-JUN-2002 (TrEMBLrel. 21, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001190; Srcr_receptor.
InterPro; IPR002155; Thiolase.
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MEDLINE-99432219; PubMed-10500163;
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EMBL; AK002694; BAB22289.1;
HSSP; P00763; 1DPO.
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Best Local Similarity 90...
9, Conservative
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1 CEGDSGGPFV 10
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Buckova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Burtis K.C., Busan D.A., Buller H., Cadleu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dodson K., Doup L.E., Downes M., Dungan-Rocha S., Dunkov B.C., Dunn P. Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.
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Adama M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adama M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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Brandon R.C., Rogers Y.-H.C., Blazel R.G., Chanpe M., Pfeilffer B.D.,
Wan K.H., Doyle C., Batter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Adril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                    "cDNA Cloning of Ovochymase, a Chymotrypsin-like Protease Released From Xenopus laevis Eggs at Fertilization.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 4 CUB DOMAINS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K.J., Evangelista C.C., Ferraz C., Ferrlera S., Fleischman
C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 13; Length 1524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Last sequence update)
Last annotation update)
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               SWART; SM00020; Tryp_SPC; 3.
PROSITE; PS01180; CUB; 5.
PROSITE; PS50240; TRYPSIN_DOM; 3.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_3.
PROSITE; PS00135; TRYPSIN_ERS; 3.
Hydrolase; Serine protease.
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                         ., Lindsay L.L., Hedrick J.L.;
                                                                                                                                                                                                                                                        InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000859; CUB_domain.
InterPro; IPR001254; Ser_protease_fry
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                                                                                                                                                                                                                                                                                                                          pfam; pr00431; CUB; 5. pfam; pr00431; CUB; 5. pfam; pr00089; trypsin; 3. PRINTS; PR00722; CHYMOTRYPSIN. SMART; SM00042; CUB; 4.
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HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                    MEROPS; S01.022; -.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          501.245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Q9V514
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A Glodek A., Gong E., Gorrell J.H., Gu Z., Guan. P., Harris M.,

A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

A Hostin D., Houston K.A., Howland T.J., Hear M..H., Iboquan C.,

A Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., Moshrefi A.,

Markulov G., Milshina N.V., Moberry C., Morris J., Moshrefi A.,

Markulov G., Milshina N.V., Moberry C., Morris J., Moshrefi A.,

Ra Malazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Spier E., Stdenfatman E., Simpson M., Strong R., Sun E.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Railiams S.M., Woodage T., Weinstock G.M., Weissenbach J.,

Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

A Glibbs R.A., Myers B.W., Rubin G.M., Venter J.C.,

Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,

A Glibbs R.A., Myers B.W., Rubin G.M., Venter J.C.,

L. Similanty TY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

THYNDEIN PARTY.
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MEDLINE-99339928; PubMed-10411621;
Yan X.-H., De Bondt H.L., Powell C.C., Bullock R.C., Borovsky D.;
Sequencing and characterization of the citrus weevil, Diaprepes
abbreviatus, trypsin cDNA. Effect of Aedes trypsin modulating oostatic
factor on trypsin blosynthesis.";
Eur. J. Biochem. 262:627-68(1999).
-1-.SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE
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Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).
Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda, Insecta;
Petrygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Phytophaga; Curculionidae; Entiminae; Entimini)
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Pred. No. 0.12;
0; Mismatches 1; Indels
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Last annotation update)
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001214; Chymotrypsin.
InterPro; IPR001224; Ser_protease_Try.
Pfan; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_LES; 1.
Hydrolase; Serine protease.
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HSSP; P00763; 1DPO.
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90.0%;
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HSSP; P00763; 1DPO.
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Best Local Similarity 90.00,
bear 9; Conservative
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21226193; PubMed-11327827;
MEDLINE-21226193; PubMed-11327827;
Takayama T.K., Carter C.A., Denny T.;
Activation of prostate-specific antigen precursor (pro-PSA) by
prostin, a novel human prostatic serine protease identified by
prostin, a novel human prostatic serine protease identified by
Biochemistry 40:1679-1687(2001).
EMBL; AF303046; AAK62813.1; -.
MEROPS; SOI.081; -.
InterPro; IPRO01254; Ser_protease_Try.
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80.0%; Pred. No. 0.12;
ive 2; Mismatches 0; Indels
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23 252 TRYPSIN.
252 AA; 26064 MW; EE0EDBF116B042AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-DEC-2001 (TrEMBLrel. 19, Created)
1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00089; trypsin; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; UNKNOWN_1.
Hydrolase; Serine protease.
SEQUENCE 255 AA: 27000.
                                                                                               DARKI; SMUUDJU; TIYP_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PYdrolase; Serine protease; Signal.
IPR001314; Chymotrypsin.
IPR001254; Ser_protease_Try.
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                                                                  PR00722; CHYMOTRYPSIN. M00020; Tryp_SPC; 1.
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Best Local Similarity 80.0
Matches 8; Conservative
                                                  fam; PF00089; trypsin; 1
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Best Local Similarity 90.0 Matches 9; Conservative

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Search completed: May 12, 2003, 15:38:38 Job time: 24.6 secs

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GenCore version 5.1.4_p5_4578
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- protein search, using sw model OM protein

May 12, 2003, 15:32:07; Search time 5.8 Seconds (without alignments) 71.511 Million cell updates/sec Run on:

US-09-909-348-1 59 Title: Perfect score:

1 CEGDSGGPFV 10 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched: 112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Score	59	59	59	59	26	26	53	53	53	. 23	53	53	53	23	. 53	53	52	52	52	52	52	51	20	50	20	20	20	20	20	20	20	200	20
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SIMILARITY

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   as its content is in
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CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAX SYSTEM (BY SIMILARITY).
CHARGE RELAX SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                     PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00114; TRYPSIN_HIS; 1.
PROSITE; PS001135; TRYPSIN_SER; 1.
Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat; Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Live:
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ACTIVATION PEPTIDE (FRAGMENT 2),
THROMBIN LIGHT CHAIN (A).
THROMBIN HEAVY CHAIN (B).
            and
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           Usage
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N-LINKED (GLCNAC. ..)
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GAMMA-CARBOXYGLUTAMIC
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GAMMA-CARBOXYGLUTAMIC
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use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See For send an email to license@isb-sib.ch).
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N-LINKED (GLCN
BY SIMILARITY.
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SIMILARITY.
SIMILARITY.
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1; GLU_CARBOXYLATION; 1.
1; KRINGLE_1; 2.
3; KRINGLE_2; 2.
                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                  InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; V1tK_dep_GIA.
                                                                                              IPR001314; Chymotrypsin. IPR002383; GLA_blood.
                                                                                                                IPR000001; Kringle.
IPR003966; Prothrombin.
                                                                                                                                                 Pram; Pr00051, kringle; 2.
Pram; Pr00051, kringle; 2.
Pram; Pr00059, trypsin; 1.
Pring; Pr00722, CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
PRINTS; PR00001; GLABLOOD.
PRINTS; PR00001; KRINGLE.
PRINTS; PR001505; RCTHROMEIN.
ProDom; PD0000395; Kringle; 2.
SWART; SM00005; GLA; 1.
SWART; SM000020; Tryp_SPC; 1.
                                               EMBL; X52835; CAA37017.1; -.
                                                         EMBL; M81397; AAA42240.1; -. PIR; S10511; S10511.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-i- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amplification and sequence analysis of the B chain of thrombin from
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6; TISSUE-Liver;
MEDLURE-91025551; PubMed-222210;
Fitzener Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
Fitzglbbon J.J., Pai J.-A., Chapman V.M., Elliott R.W.;
"Characterization of the cDNA coding for mouse prothrombin and localization of the gene on mouse chromosome 2.";
DNA Cell Biol. 9:487-498(1990).
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                                                                             DB 1; Length 617; 0.0062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Banfield D.K., Macgillivray R.T.; "Partial characterization of vertebrate prothrombin cDNAs:
                                                                                                      Indels
           SIMILARITY).
                                                        AD27D1B71445DB1D CRC64;
                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
101-NOV-1990 (Rel. 16, Last sequence update)
101-NOV-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.21.5).
        INTERCHAIN (BY S
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                             618 AA
                                                                            100.0%; Score 59; DE
100.0%; Pred. No. 0.(
Live 0; Mismatches
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MEDLINE-92212913; PubMed-1557383;
                                 BY
BY
                                                        70411 MW;
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                                                                                         larity 100.0%;
Conservative 0
                                                                                                                                                                                                             STANDARD;
287
478
403
546
590
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264
332
387
532
560
617 AA;
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                                                                                           Local Similarity
nes 10; Conserv
                                                                                                                            1 CEGDSGGPFV 10
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                             DR PROSITE; PS00011; Tryp_SPc; 1.

DR PROSITE; PS00011; GIU_CARBOXYLATION; 1.

DR PROSITE; PS00021; KRINGLE_1; 2.

DR PROSITE; PS50070; KRINGLE_2; 2.

DR PROSITE; PS00134; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_DOM; 1.

DR PROSITE; PS00135; TRYPSIN_LES; 1.

WAYLEAUIN K; Zymogen; Gamma-carboxyglutemic acid; Acute phase; Liver; W Yltamin K; Zymogen; Gamma-carboxyglutemic acid; Acute phase; Liver; W Hydrolase; Serine protease; Kringle; Signal.

T SIGNAL

T PROPEP 25 1.
                                                                                                                                                                                                                                                                                                                                      CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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ACTIVATION PEPTIDE (FRAGMENT
THROMBIN LIGHT CHAIN (A)
THROMBIN HEAVY CHAIN (B)
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                                       PROTHROMBIN.
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                                                                                                                                       Pfam; PP00594; gla; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
PRINTS; PR01505; RRINGLE.
PRINTS; PR01505; PROTHROMBIN.
PRODOM; PD000395; Kringle; 2.
SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_SPC; 1.
                                                                                                                           Pfam; PF00051; kringle; 2.
Pfam; PF00089; trypsin; 1.
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SEQUENCE OF 8-622 FROM N.A.
MEDLINE-83231469; PubMed-6305407;
Degen S.J.F., McGillivray R.T.A., Davie E.W.;
"Characterization of the complementary deoxyribonucleic acid and gene
                                                                                                                                                                                                                                                    Gaps
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MEDLINE-90059942; PubMed-2583108;
Bode W., Mayr I., Baumann U., Huba. R., Stone S.R., Hofsteenge J.;
"The refined 1.9 A crystal structure of human alpha-thrombin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Prothrombin fragment 1 X 2 X 3, a major product of prothrombin activation in human plasma.";
J. Biol. Chem. 261:13210-13215(1986).
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Butkowski R.J., Elion J., Dowahlog M.R., Mann K.G.;
"Primary structure of human prethrombin 2 and alpha-thrombin.";
J. Biol. Chem. 252:4942-4957(1977).
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Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.
Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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1-JUL-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II)
                                                                                                                                                                                                  Length 618;
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                                                                                                                                                                               Score 59; DB 1; Length ox. Pred. No. 0.0062;
                                                                                                                                    N-LINKED (GLCNAC. . .).
B89F719AAFD601E0 CRC64;
                                                                N-LINKED (GLCNAC...).
N-LINKED (GLCNAC...).
N-LINKED (GLCNAC...).
BY SIMILARITY.
BY SIMILARITY.
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MEDLINE-87008532; PubMed-3759958;
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Biochemistry 22:2087-2097(1983)
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547
591
122
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Best Local Similarity 100.
Matches 10; Conservative
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618 AA;
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CARBOHYD
    DISULFID
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<u>:</u>
          Cera E.;
interaction with D-Phe-Pro-Arg chloromethylketone and significance of
the Tyr-Pro-Pro-Trp insertion segment.";
EMBO J. 8:3467-3475(1989).
                                                                                                                                                                                                                                                                                                              X-RAI CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE-94350942; PubMed-8071320;
Rydel T.J., Yin M., Padmenabhan K.P., Blankenship D.T., Cardin A.D.,
Correa P.E., Fenton J.W. II, Tulinsky A.; Crystallographic structure of human gamma-thrombin.";
J. Blol. Chem. 269:22000-22006(1994).
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Rabiet M.-J., Furie B.C., Furie B.;
"Molecular defect of prothrombin Barcelona. Substitution of cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
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"Identification of the primary structural defect in the dysthrombin thrombin Quick I: substitution of cysteine for arginine-382.";
Blochemistry 27:9160-9165(1988).
                                                                                                                                                                                                                "The structure of a complex of recombinant hirudin and human alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Esmon C.T., Stubbs M.T.;
"The thrombin E1920-BPII complex reveals gross structural
transangements: implications for the interaction with antithrombin
and thrombomodulin.":
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Prothoroubln Frankfurt: a dysfunctional prothrombin characterized
substitution of Glu-466 by Ala ";
Thromb. Haemost. 73:203-209(1995).
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Guinto E.R., Caccia S., Rose T., Fuetterer K., Waksman G., di C
"Unexpected crucial role of residue 225 in serine proteases.";
Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
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                                                                                                                                 MEDLINE-90327074; PubMed-2374926;
Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber
Roltsch C., Fenton J.W. II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-97357286; PubMed-9214615;
Van de Locht A., Bode W., Huber R., le Bonniec B.F., Stone
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MEDLINE-95169898; PubMed-7865694;
MEDLINE-18KE-18KIM D.-0., Girolami A.;
James H.L., Kim D.J., Zheng D.-0., Girolami A.;
Jerochrombin Padua I: incomplete activation due to substitution at a factor Xa cleavage site.;
Blood Coagul. Fibrinolysis 5:841-844(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
                                                                                                            X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for arginine at residue 273.";
J. Biol. Chem. 261:15045-15048(1986).
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MEDLINE-93043342; Pubmed-1421398;
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MEDLINE-89247398; PubMed-2719946;
Henriksen R.A., Mann K.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 16:2977-2984(1997).
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Blood 80:2275-2280(1992).
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  REPRESENTATION OF THE PRESENTATION OF THE PRES
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PEPTIDES, WITH ADDITIONAL CLEAVAGE AFTER 314-ARG, ARE RELEASED IN NATURAL BLOOD CLOTTING.
MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION BY FACTOR XA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANGOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN & PACTORS AS & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES THE ACTIVATION PEPTIDE & CIEAVES THE REMAINING PART INTO LIGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWIX BECAUGE FACTOR VITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
"Substitution of valine for glycine-558 in the congenital dysthrombin thrombin Quick II alters primary substrate specificity."; Blochemistry 28:2078-2082(1989).
                                                                                                                                                            "Prothrombin Salakta: substitution of glutamic acid-466 by alanine reduces the fibrinogen clotting activity and the esterase activity."; Blochemistry 31:7457-7462(1992).
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                                                                                                                                                                                                                                                                                                                           "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan that impairs the fibrinogen clotting activity of derived thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inomoto T., Shirakami A., Kawauchi S., Shigekiyo T., Saito S., Miyoshi K., Morita T., Iwanaga S.; Prothrombin Tokushima: characterization of dysfunctional thrombin derived from a variant of human prothrombin."; Blood 69:565-569(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Iwahana H., Yoshimoto K., Shigekiyo T., Shirakami A., Saito S., Itakura M.;
                                                                                                                                                                                                                                                                  MEDLINE-87185407; PubMed-3567158;
Miyata T., Morita T., Inomoto T., Kawauchi S., Shirakami A.,
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                                                                                                                      Miyata T., Aruga R., Umeyama H., Bezeaud A., Guillin M.-C.,
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MISCELLANEOUS: IT IS NOT KNOWN WHETHER 1
                                                                                                   MEDLINE-92378975; PubMed-1354985;
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1ETR; 31-JAN-94
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PIR; S02537; S02537.
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Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
"The structure of residues 7-16 of the A alpha-chain of human
fibrinogen bound to bovine thrombin at 2.3-A resolution.";
J. Biol. Chem. 267:7911-7920(1992).
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Soriano-Garcia M., Padmanabhan K., de Vos A.M., Tulinsky A.;
The Ca2+ ion and membrane binding structure of the Gla domain of Ca-
                                               Gaps
 DOES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 44-625, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES. Magnusson S., Sottrup-Jensen L., Petersen T.E., Claeys H.; (In) Henker H.C., Veltkamp J.J. (eds.); Boerhaeve symposium on prothrombin and related coagulation factors, pp.25-46, Leiden University Press, Leiden (1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Park C.H., Tulinsky A.; "Three-dimensional structure of the kringle sequence: structure of prothrombin fragment 1.";
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDILE-842.032.5; pubmed-6326805; MEDILE-842.032.5; pubmed-6326805; MCGillivray R.T.A. Davie E.W.; "Characterization of bovine prothrombin mRNA and its translation
-I- MISCELLANEOUS: THE CLEAVAGE AFTER R-198, OBSERVED IN VITRO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91311686; Pubmed-1856869;
Seshadri T.-P., Tulinsky A., Skrzypczak-Jankun E., Park C.H.;
"Structure of bovine prothrombin fragment 1 refined at 2.25-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF ACTIVATION PEPTIDE 1
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                       Length 622;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-88245190; PubMed-3379642;
Trufn D.M., Robertson K.A., Macgillivray R.T.A.;
"Structure and evolution of the bovine prothrombin gene.";
J. Mol. Biol. 200:31-45(1988).
                                               Indels
                      Query Match 100.0%; Score 59; DB 1; L. Best Local Similarity 100.0%; Pred. No. 0.0062; Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-APR-1990 (Rel. 14, Last sequence update)
12-JUN-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.21.5).
                                                                                                                                                          625 AA.
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                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prothrombin fragment 1.";
Blochemistry 31:2554-2566(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 25:3977-3982(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                               iochemistry 23:1626-1634(1984).
                                                                                                                                                          STANDARD;
                                                                                   111111111
564 CEGDSGGPFV 573
                                                                                                                                                                                                                                            taurus (Bovine)
                                                                       1 CEGDSGGPFV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANBOORS: PROTHROWBIN IS ACTIVATED ON THE SURFACE OF A PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN & PACTORS AS A XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT & HEAVY CHAINS, THE ACTIVATION PROCESS STARTS SLOWLY BECANGE FACTOR V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN. MEDLINE-97102783; PubMed-8947023; van de Locht A., Stubbs M.T., Bode W., Friedrich T., Bollschweiler C., Hoffken W., Huber R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION BY FACTOR XA.
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-92389319; PubMed-1518046;
Brandstetter H., Turk D., Hoeffken H.W., Grosse D., Stuerzebecher J.,
Martin P.D., Edwards B.F.P., Bode W.;
"Refined 2.3 A X-ray crystal structure of bovine thrombin complexes
                                                                                                                                                            formed with the benzamidine and arginine-based thrombin inhibitors NAPAP, 4-TAPAP and MOPA. A starting point for improving antithrombotics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huber R., Bode W.;
Structure of the thrombin complex with triabin, a lipocalin-like
"Structure of the inhibitor derived from a triatomine bug.";
Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-TAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIABIN.
MEDLINE-98004486; PubMed-9342325;
Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schleuning W.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-1- SIMILARITY: COWTAINS 2 KRINGLE DOMAINS.
-1- DATABASE: NAME-PROSYME technical fact sheet;
WWW-"http://www.prozyme.com/technical/thrombindata.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The ornithodorin-thrombin crystal structure, a key to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          J. Mol. Biol. 226:1085-1089(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enigma?";
EMBO J. 15:6011-6017(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease; Transmembrane; Signal-anchor.

1 161 NON-CATALYTIC CHAIN (POTENTIAL).

162 416 CATALYTIC CHAIN (POTENTIAL).

1 16 CYTOPLASMIC (POTENTIAL).

17 43 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                             protease, hepsin, from mouse preimplantation embryos.";
J. Biol. Chem. 272:31315-31320(1997).
-!- FUNCTION: PLAYS AN ESSENTIAL ROLE IN CELL GROWTH AND MAINTENANCE
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
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BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

432194FP4004B848 CRC64;
                                                                                                                                                                                                                                                                                                  TISSUE-Liver;
MEDITE-9805912; PubMed-9395459;
W I.-K.H., Liu R.W., Haaksma C., Tomasek J.J., Howard E.W.;
"Identification and cloning of the membrane-associated serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine protease hepsin (EC 3.4.21.-).
                                                                                               416
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MGD; MGI:1196620; Hpn.
InterPro; IPR001214; Chymotrypsin.
InterPro; IPR001214; Chymotrypsin.
InterPro; IPR001314; Ser_protease_Try.
InterPro; IPR00130; Src_receptor.
Pfam; PF00089; trypsin; 1.
SMART; SM00202; SR; 11.
SMART; SM00202; SR; 11.
PROSITE; PS50240; TRYPSIN_LDOM; 1.
PROSITE; PS00134; TRYPSIN_LSE; 1.
PROSITE; PS00134; TRYPSIN_LSE; 1.
Hydrolase; Serine protease; Transmembran.
                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF030065; AAB84221.1; -. HSSP; P00763; 1DPO.
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                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              OF CELL MORPHOLOGY
                                                                                                                                                                                                         Mus musculus (Mouse)
 111111111
567 CEGDSGGPFV 576
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                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      NCBI_TaxID-10090;
                                                                                           HEPS_MOUSE
035453;
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DISULFID
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SEQUENCE
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TRANSMEM
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                                                                                HEPS_MOUSE
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                                                                                               SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00011; GLU_CARBOXILATION; 1.
PROSITE; PS00011; KRINGLE_1; 2.
PROSITE; PS50070; KRINGLE_2; 2.
PROSITE; PS50070; TRYPSIN_DOW; 1.
PROSITE; PS500134; TRYPSIN_HIS; 1.
BLOOD COAGULATION; Plasma; Calclum-binding; Glycoprotein; Repeat; Vitamin K; Zmogen; Gamma-carboxyglutamic acid; Acute phase; Liver; Signal, Serine protease; Kringle; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100.0%; Score 59; DB 1; Length 625; Similarity 100.0%; Pred. No. 0.0063; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATION PEPTIDE (FRAGMENT ACTIVATION PEPTIDE (FRAGMENT THROMBIN LIGHT CHAIN (A).
THROMBIN HEAVY CHAIN (B).
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GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
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CLEAVAGE (BY THOMBIN).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CLARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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GAMMA-CARBOXYGLUTAMIC
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KRINGLE 2.
                                                                                                                                                                                                                                                                              InterPro; IPR000001; Kringle.
InterPro; IPR003966; Prothrombin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; Vitk_dep_GIA.
PF00051; Kringle; 2.
                                                                                                                                                                                                                                                  Chymotrypsin.
GLA blood.
                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0001; GLABLOOD.
PRINTS; PRO1505; PROTHROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD000395; Kringle; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00069; GLA; 1
SMART; SM00130; KR; 2.
                                                                                                                                                                    21-APR-97.
06-MAY-98.
                                                                                                                                                                                                   17-JUN-98.
16-FEB-99.
                                             31-JAN-94
31-JAN-94
                                                                                                                                                                                                                                                 IPR001314;
                                                                                                                         14-0CT-96
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                                                                                                          07-JUL-97
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Best Local Simi
Matches 10;
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Gaps

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Score 56; DB 1; Length 416; Pred. No. 0.014; 1; Mismatches 0; Indels

94.9%; illarity 90.0%; Conservative

Similarity 9; Conserva

Query Match Best Local S Matches

Gaps

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Indels

TRYPSIN_DOM; 1. TRYPSIN_HIS; 1. TRYPSIN_SER; 1.

us-09-909-348-1.rsp

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PROSITE; PS50240;
PROSITE; PS00134;
PROSITE; PS00135;
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TOTICS-ROSAGO A., O'Shea K.S., Tsuji A., Chou S.H., Kurachi K.;
"Repsin, a putative cell-surface serine protease, is required for mammalian cell growth.";
Proc. Natl. Acad. Sci. U.S.A. 90:7181-7187(1993).
-i- FUNCTION: PLAY$ AN ESSENTIAL ROLE IN CELL GROWTH AND MAINTENANCE
                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-UNV-2002 (Rel. 41, Last annotation update)
Serine protease hepsin (EC 3.4.21.-) (Transmembrane protease, serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leytus S.P., Loeb K.R., Hagen F.S., Kurachi K., Davie E.W.;
An ovel trypsin.llke serine protease (hepsin) with a putative
Transmembrane domain expressed by human liver and hepatoma cells.";
Blochemistry 27:1067-1074(1988).
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-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: PRESENT IN MOST TISSUES, WITH THE HIGHEST LEVEL IN LIVER.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choù S.H., Kurachi K.;
"Hepsin, a cell membrane-associated protease. Characterization,
tissue distribution, and gene localization.";
J. Blol. Chem. 266:16948-16953(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isuji A., Torres-Rosado A., Arai T., le Beau M.M., Lemons R.S.
                                                                                                                                                                                                                                                                                                                                               417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001190; Srcr_receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
MEDLINE-91358502; PubMed-1885621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-88209431; PubMed-2835076;
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PRINES, PR00722; CHYMOTRYPSIN.
SMART; SM00202; SR; 1.
SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                  348 COGDSGGPFV 357
                                                    CEGDSGGPFV 10
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                                                                                                                                                                                                                                                                                                                                          HEPS_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                          P05981;
                                                                                                                                                                                                                                                                                                        HEPS_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                          PARTER BENEFIELD BENEFIELD
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                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protesse; Transmembrane; Signal-anchor.

1 162 NON-CATALYTIC CHAIN (POTENTIAL).
153 417 CATALYTIC CHAIN (POTENTIAL).
1 17 CYTOPIASMIC (POTENTIAL).
18 44 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1999 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
14-UN-2002 (Rel. 41, Last annotation update)
(Vitamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1. CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                          SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL)
B2086FF661E551D7 CRC64;
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                               Score 56; DB 1; Length 417;
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and VIIIa.
-1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 AA
                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                       45011 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D43751; BAA07808.1; -. HSSP; P04070; 1PCU.
                                                                                                                                                                                                                                                                                    94.98;
                                                                                                                                                                                                                                                                                                   90.06;
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                        204
338
381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                   1:1111111
349 CQGDSGGPFV 358
                                                                                                                                                                                                                                        112
417 AA;
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  1 CEGDSGGPFV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S01.218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRTC_CANFA
Q28278;
                                                                                                                                                                                                                                                                                                                     ..
6
    Hydrolase;
                                                                                                                            ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                      DISULFID
CARBOHYD
SEQUENCE
                                                  DOMAIN
TRANSMEM
                                                                                                                                                                           DISULFID
                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                          DISULFID
                                                                                                DOMAIN
                                                                                                                OMAIN
                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRTC_CANFA
                                                                                                                                                                                                                                                                                                                     Matches
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us-09-909-348-1.rsp

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PRTC_FELCA
                  DISULFID
CARBOHYD
CARBOHYD
ACT_SITE
DISULFID
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DISULFID
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SEQUENCE
                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARBOHYD
                                                                                                                                                                                        028412;
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                                               NON_TER
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                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2004 (Rel. 41, Last annotation update)
Vitamin R dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Capra.
                                            CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROFS; SO1.218; --
InterPro; IPR001254; Ser_protease_Try.
Fran, PF00009; tryps.nr, 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; PARTIAL.
BROSITE; PS00135; TRYPSIN_LIS; 1.
Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
                           Blood coagulation, Glycoprotein, Serine protease, Hydrolase, NON_TER 1
                                                                                                                              Score 53; DB 1; Length 157;
Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
                                                                                                                                                  1; Indels
                                                                                                              17262 MW; E8B1BACF49220DFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                     157 AA
                                                                                                                                                 0; Mismatches
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                              89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D43752; BAA07809.1; -. HSSP; P04070; 1PCU.
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                              Capra hircus (Goat).
                                                                                  17
78
157
157 AA;
                                                                                                                                                                                       121 CEGDSGGPMV 130
                                                                                                                                                                     1 CEGDSGGPFV 10
                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-9925;
                                                                                                                                                 9,
                                                                                                                                                                                                                                     PRTC_CAPHI
Q28315;
                                             ACT_SITE
ACT_SITE
DISULFID
DISULFID
CARBOHYD
                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                             PRTC_CAPHI
                                                                                                                                                 Matches
RARATTTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Felis silvestris catus (Cat).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp.SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS500134; TRYPSIN_LEM; 1.
PROSITE; PS00135; TRYPSIN_SR; 1.
Blood_coagulation; Glycoprotein; Serine protease; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                              1; Indels
                                                                                                                                               B89790F9954B610A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17142 MW; FBDC5BE2ECA74BB4 CRC64;
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                              Score 53; DB 1;
Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 AA.
                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                               17251 MW;
                                                                                                                                                                                            89.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D43750; BAA07807.1; -.
                                                                                                                                                                   Ouery Match
Best Local Similarity 90...
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                       121 CEGDSGGPMV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
78
157
157 AA;
                                                                                                                                                 157 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P04070; 1PCU.
                                                                                                                                                                                                                                                                                      1 CEGDSGGPFV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÆROPS; S01.218;
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121 CEGDSGGPMV 130

Length 157;

PRTC_HORSE Q28380;

PRTC_HORSE RESULT 10

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994).
-i- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAI REGULATES BLOOD COAGLIATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94318474; PubMed-8043441;
Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
                                                                                                                               15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                                                                                 Macaca mulatta (Rhesus macaque).
Bukaryota: Metazoa; Chordata; Graniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.8%; Score 53; DB 1; Length 161; 90.0%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27D78F185B2FCC69 CRC64;
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CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z
                                                                                              161 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSS0240; TRYPSIN DOM; 1.
PROSITE; PSO0134; TRYPSIN HIS; PARTIAL.
PROSITE; PSO0135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT:
                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D43754; BAA07811.1; -. HSSP; P04070; 1PCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 CEGDSGGPMV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CEGDSGGPFV 10
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS: S01,218;
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and VIIIa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
KLKF_HUMAN
ID KLKF_HUMAN
                                                                                              PRTC_MACMU
Q28506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994).
-!- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                             Gaps
                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
Anticoagulant protein C (S 1000 coagulation factor XIV) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94318474; PubMed-8043441;
Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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Pred. No. 0.018;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BFAA6EA045C3C580 CRC64;
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                   DB 1;
0.018;
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SIMILARITY.
                                                             Mismatches
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Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1.
                   Score 53;
Pred. No.
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90.0%;
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                   89.8%;
90.0%;
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                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           caballus (Horse)
Query Match
Best Local Similarity
'-hag 9; Conserv?
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9; Conserv
                                                                                                                                              121 CEGDSGGPMV 130
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                                                                                                       1 CEGDSGGPFV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9796;
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Query Match Best Local S

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(KLK-L4).
KLK13 OR KLKL4.
                  VARSPLIC
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CONFLICT
SEQUENCE
CARBOHYD
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                                                                                                                                                                                                                                                             PubMed-11010966;
Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.P.;
Molecular clonding of the human kallikrein 15 gene (Kikl5). Uprequilation in prostate cancer.";
J. Biol. Chem. 276:53-61(2001).
                                                                                                                                                                              Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCualg J., Moss P., Paeper B., Wang K.; Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; Gene 257:119-130(2000).
                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVATION PEPTIDE (POTENTIAL).
KALLIKREIN 15.
       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Rallikrein 15 precursor (EC 3.4.21.-) (ACO protease).
Q9H2R6; Q9H2R4; Q9H2R3; Q9HBG9; Q15358;
                                                                                                                                                                                                                                    PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-20510030; PubMed-11054574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X75363; CAA53145.1; ALT_SEQ.
HSSP; P00763; 1DPO.
MEROPS; S01.081; -.
                                                                                                                                                                                                                                                      MEDLINE-94289486; PubMed-8018728;
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF242195; AAG09469.1; -. EMBL; AF242195; AAG09470.1; -. EMBL; AF242195; AAG09471.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF242195; AAG09472.1; -
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                                                      Homo sapiens (Human)
                                                                              NCBI_TaxID-9606;
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                                             KLK15.
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Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Valasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDIJNE-20229789; PubMed-10766816;
Yousef G.M., Chang A., Diamandis B.P.;
Identification and characterization of KLK-L4, a new kallikrein-like gene that appears to be down-regulated in breast cancer tissues.";
J. Biol. Chem. 275:11891-11898(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIKD HUMAN STANDARD; PRT; 2// An. 09V433; 09V433; 06C-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41). Last annotation update) 15-JUN-2002 (Rel. 41). Last annotation update) Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-like protein 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ansorge W., Wirkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELDILAR LOCATION: Secreted (Probable).
-!- TISSUE SPECIFICITY: EXPRESSED IN PROSTATE, BREAST, TESTIS AND SALIVARY GLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                       SHNEPGTAGSPRSQ -> PLSSP (IN REF. 2)
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                               89.8%; Score 53; DB 1; Length 256; 90.0%; Pred. No. 0.029; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                    B5EBF8D6022786B5 CRC64;
                                                              MISSING (IN ISOFORM 4)
MISSING (IN ISOFORM 2)
                                                                                                                     V -> G (IN ISOFORM 3).
MISSING (IN ISOFORM 3)
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EMBL; AC01147; AAC3259.1; -.
EMBL; AC01202; CAB43320.1; ALT_INIT.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                       MW;
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                                                                                                                                                                                                                       28087
                                                                                                                                                                                                                                                                                                                                                9; Conservative
   171
232
206
256
161
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160
171
232
122
122
161
162
147
256 AA;
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205 CEGDSGGPLV 214
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Best Local Similarity
Matches 9; Conserv
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PF00089;
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                                                                                                       PROCESSING
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MEDLINE-85014826; Pubmed-6091100;
Long G.L., Balagaje R.M., McGillivray R.T.A.;
"Cloning and sequencing of liver cDNA coding for bovine protein C.";
Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
VNYPKTLQCAN -> GMHPHRWPEAP (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987 (Rel. 05, Last sequence update)
15-UDN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C precursor (BC 34.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Sukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                  SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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MEDLINE-83007325; PubMed-6896876;
Fernlund P., Stenflo J., Stenflo J., Shanno acid sequence of the light chain of bovine protein C.";
J. Biol. Chem. 257:12170-12179(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-83169769; PubMed-6572939;
Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                            Score 53; DB 1; Length 277; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                1; Indels
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(BY
(BY
                                                                                                                                 CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                      SMAKI; SMOUGAO, INFL-CT.
PROSITE; PS50240; TRYPSIN.DOM; 1.
PROSITE; PS00134; TRYPSIN.LHS; 1.
PROSITE; PS00135; TRYPSIN.SER; 1.
Hydrolase; Serine protease; Glycoprotein; Signal.
STRANI.
                                                                                                                                                                                                                                                                                                                                                                    456 AA.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                         KALLIKREIN 13.
                                                                                                                                                                                                                                                                                0; Mismatches
                           InterPro: IRR001314; Chymotrypsin.
InterPro: IRR001254; Ser_protease_Try.
Pfam; PF00009; trypain; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp_SPC; 1.
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MEDLINE-83007326; PubMed-6896877;
                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                           30570 MW;
                                                                                                                                                                                                                                                             89.8%;
90.0%;
                                                                                                                                                                                                                                                                                9; Conservative
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         HGNC: 6361; KLK13.
                                                                                                                                                                                                                                                                                                                                                                                                                                    actor XIV) (Fragment)
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214 CEGDSGGPLV 223
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                                                                                                                                                                                                                                          277 AA;
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                     605505;
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ACT_SITE
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-1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.

-1- FINH: THE VITAMIN K-DEPENDENT; ENXTMATIC CARBOXYLATION OF SOME GLO RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.

-1- MISCELLANDEOUS; CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBOMODULIN COMPLEX.
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Gamma-carboxyglutamic acid; Calcium-binding; Vitamin R; Hydroxylation;
EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-83213513. PubMed-6304092;
Esmon N.L., Debault L.E., Esmon C.T.;
*Profeolytic formation and properties of gamma-carboxyglutamic acid-
amminian motion for the contraction of the 
Stenflo J., Fernlund P.; "Amino acid sequence of the heavy chain of bovine protein C."; J. Biol. Chem. 257:12180-12190(1982).
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PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00011; GLU_CARDANCLATION; 1.
PROSITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
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SMART; SM00069; GLA: 1.
SMART; SM00020; TYP_SPC: 1.
PROSITE; PS00010; ASK_HVDROXYL; 1.
PROSITE; PS00022; EGF_1: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blood coagulation; Glycoprotein; Serine protease;
Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
GGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
SIGNAL 1 BY SIMILARITY.
PROPEP 19 41 BY SIMILARITY.
CHAIN 42 459 VITAMIN K-DEPENDENT PROTEIN C.
CHAIN 42 196 SIMILARITY.
                                                                               Cell. Mol. Life Sci. 58:148-159(2001).
-!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                         *Porcine factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN C HEAVY CHAIN (BY SIMILARITY). A STATIVATION PEPTIDE (BY SIMILARITY). CLEAVAGE (BY THROMBIN) (BY
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PROSITE; PS00021; BGF_1; 1.
PROSITE; PS010021; BGF_2; 2.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00111; GLU_CARBOXYLATION; 1.
PROSITE; PS00214; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
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InterPro: IPR00152; Asx_hydroxyl.
InterPro: IPR001512; Asx_hydroxyl.
InterPro: IPR001814; Chymctrpsin.
InterPro: IPR001881; EGF-Ia.
InterPro: IPR001881; EGF-Ca.
InterPro: IPR001284; SGT_blood.
InterPro: IPR001284; VItK_dep_GIA.
Pfam; PF00008; EGF: 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00701; GLABLOD.
SMART; SM00181; EGF: 2.
SMART; SM00001; GLABLOD.
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MEDLINE-21121490; PubMed-11229814;
Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
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16-OCT-2010 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin R dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Pred. No. 0.052;
0; Mismatches 1; Indels
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prostate specific antigen; PSA; epitope; monoclonal antibody;
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The present sequence represents a prostate specific antigen (PSA)

Chem Horoclonal antibodies specific for PSA and hybridomas producing peptide. Monoclonal antibodies: (a) bind to free PSA; (b) are monoclonal antibody 365 binding to amino acids 82-87 of free PSA; (b) are monoclonal antibody 82-87 of free PSA; (b) are monoclonal antibodies 10, 11, 16 or 22.2 and 15.2, 156 or 22.5 binding to amino acids 139-144 (EEEETP) and 55-60

C(SIFHPE) respectively of free and bound PSA, or fragments. The antibodies are useful to detect PSA. For detecting free PSA only, an immunoassay comprising a solid support with attached labelled monoclonal antibody specific for free PSA (especially (b)) and a PSA standard can be used.

Cofficiently labelled) monoclonal antibody binding free and bound PSA (especially prostate and bound PSA, a second solid support with attached (afferently labelled) monoclonal antibody binding free and bound PSA (especially prostate from (c)) can be used either with, or in place of, the first solid support. The antibodies are useful in cancer screening, especially prostate and breast cancer. By obtaining total and free PSA (alferent prostate chome) patients. Measurement of PSA is also useful after radical prostatectomy, to predict disease persistence. The antibodies allow evaluation of PSA free/total radio, enabling separation of PSA free/total radio, enabling separation of possible by total PSA testing, avoiding biopsies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; prostate specific antigen; PSA; epitope; monoclonal antibody; detection; cancer; serine protease.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 19; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate specific antigen peptide SEQ ID NO:80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 10;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW58062 standard; peptide; 15 AA.
                                   Example; Page 63; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US14909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0025404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-193789/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXGDSGGPXV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 CSGDSGGPLV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AA;
 prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9810292-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heavner GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW58062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
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Monoclonal antibodies specific for prostate specific antigen useful, e.g. in screening for prostate or breast cancer and especially to distinguish between benign prostatic hyperplasia and

Example; Page 63; 84pp; English

prostate cancer

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The present sequence is presented a prostite of the managem (FSA) and hybridomas producing them have been developed. The antibodies: (a) bind to free PSA: (b) are monoclonal antibody 565 binding to amino acids 82-87 of free PSA: (b) are monoclonal antibody 81-87 of free PSA: (b) are monoclonal antibodies 10, 11, 16 or 22.2 and conference of tragment, and (c) are monoclonal antibodies 10, 11, 16 or 22.2 and conference of the monoclonal antibodies are useful to detect PSA. For detecting free PSA only, an immunoassay comprising a solid support with attached labelled monoclonal antibody specific for free PSA (especially (b)) and a PSA standard can be used. To detect both free and bound PSA, a second solid support with attached (alferently labelled) monoclonal antibody binding free and bound PSA (especially selected from (c)) can be used either with, or in place of, the first solid support. The antibodies are useful in cancer screening, capecially prostate and breast cancer. By obtaining total and free PSA values, their ratio can be used to separate prostatic cancer (PCa) from consensing the prostatic hyperplasia (BHP) patients. Measurement of PSA is also useful after radical prostatectomy to predict disease persistence. The cutbodies allow evaluation of PSA free/fotal ratio, enabling separation of BPH and PCA patients with PSA values 4-10 ng/ml not previously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a novel peptide which has 20 contiguous amino acids derived from the 240 residue sequence of the human prostate specific antigen (PSA) (see AAM1023). The preferred peptide has two hydrophobic regions and one hydrophilic region each of about 5 as in length, arranged as follows: hydrophobic-hydrophilic-hydrophobic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen peptide derived from prostate specific antigen - does not cross react with related kallikreins, for diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSA; kallikrein; prostate cancer; antigenic; polyclonal antisera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen peptide derived from human prostate specific antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 19; Length 15;
Pred. No. 10;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kokolus WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 42; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW11019 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXGDSGGPXV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36-JUN-1996;
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us-09-909-348-2.rag

160 CSGDSGGPLV 169

AAR84671 standard; Protein; 237 AA.

serine protease; prostate-specific antigen;

prostate cancer; diagnosis.

Homo sapiens WO9530758-A1

Kallikrein hK3;

Mature kallikrein hK3

04-MAR-1996

AAR84671;

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABBS7737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.Wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions .
Polyclonal antisera specific for the antigenic peptide may be used in method for diagnosing prostate cancer in vivo or in vitro. The peptide represents a sequence unique to PSA which does not cross react with certain kallikreins.
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 25644; 21pp + Sequence Listing; English.
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                                                                                                                Score 47; DB 18; Length 20;
Pred. No. 13;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 25644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers EW;
                                                                                                                                                                                                                                                                                               ABB66284 Standard; Protein; 214 AA.
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                                                                                                              94.0%;
nilarity 80.0%;
Conservative 0,
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Best Local Similarity 80.0%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75
                                                                                                                                 Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                 1 CXGDSGGPXV 10
                                                                                                                                                                                                      4 CSGDSGGPLV 13
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                                                                                   20 AA;
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                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
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                                                                                                                                                                                                                                                                                                                              ABB66284;
                                                                                     Sequence
                                                                                                                   Query Match
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ABB66284
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Young CYF;

Tindall DJ,

Saed! MS,

WPI; 1995-404123/51.

95US-0427767.94US-0241174. 95WO-US06157

02-MAY-1995; 10-MAY-1994;

09-MAY-1995;

16-NOV-1995

(HYBR-) HYBRITECH INC. (MAYO-) MAYO FOUNDATION.

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Gaps
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                                                                                                 Human kallikrein hK3 (AAR84671) is a prostate-specific kallikrein showing homology to prostate-specific glandular kallikrein hK2 (AAR84667). Nonhomologous regions of the kallikreins can be used for prepn. of antibodies specific to hK2.
New isolated prostate-specific kallikrein polypeptide(s) - used to develop prods. for use in assays for such polypeptide(s), partic. for diagnosis and monitoring of prostate cancer
                                                                                                                                                                                                                                                                    ő
                                                                                                                                                                                                                               94.0%; Score 47; DB 16; Length 237; 80.0%; Pred. No. 84; 2; Indels ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate-specific antigen; prostate cancer; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                              AAR77098 standard; Protein; 237 AA.
                                                                         Disclosure; Page 31; 61pp; English:
                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                             | |||||| |
185 CSGDSGGPLV 194
                                                                                                                                                                                                                                                                                                       1 CXGDSGGPXV 10
                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                            237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09528498-A1
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                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                 Query Match
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Gaps

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1 CXGDSGGPXV 10

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(CENZ ) CENTOCOR INC
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                                                                                                                                             185 CSGDSGGPLV 194
                                                                                                                            1 CXGDSGGPXV 10
                                                                       237 AA;
                                                                                                                                                                                                                                                                 prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer
                                                                                                                                                                                                                                                                                                            WO9810292-A1
                                                                                                                                                                                                                                                                                            Homo saplens
                                                                                                                                                                                                                            11-AUG-1998
                                                                                                                                                                                                                                                                                                                                                25-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                 06-SEP-1996;
                                                                                                                                                                                                                                                                                                                              12-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                     Heavner GA:
                                                                                                                                                                                                          AAW56086;
                                                                        Sequence
                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                        RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a diagnostic method for detecting human stallikrein 2 (kT2) DNA. The method comprises: (a) contacting DNA obtained by reverse transcription (RT) of RNA from a human physiological sample which comprises cells suspected of containing hK2 RNA with at least 2
                                                                                                                                                  A prostate-specific antigen (PSA) is detected by isolating mRNA from a sample, producing cDNA, and subjecting the cDNA to RT-PCR using primers specific for the human PSA coding region (given in AAT04864).
                                                                                                                                                                                                                            Gaps
                                                                                                        Method for enhancing prostate-specific antigen detection - provides sensitive means to identify early stages of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                Prostate cancer; detection; hK2; hK1; hK3; phK2; tissue kallikrein; pphK2; prostate-specific glandular kallikrein protein; PSA; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of human kallikrein 2 RNA - by reverse transcription amplification by PCR, for detecting, monitoring and staging of
                                                                                                                                                                                                         16; Length 237;
                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                      DB 7
84;
                                                                                                                                                                                                         Score 47; DB 1
Pred. No. 84;
0; Mismatches
                                                              Raffo A;
                                                                                                                                                                                                                                                                                                                                                               Prostate-specific antigen protein hK3.
                                                                                                                                 Disclosure; Page 69-70; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Young CYF;
                                                                                                                                                                                                                                                                                                            Ź
                                                              Olsson CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 90pp; English.
                                                                                                                                                                                                                                                                                                         AAW83213 standard; Protein; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                           ö
                                           (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                         94.0%;
80.0%;
        95WO-DS04680
                          94US-0229391,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0843076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US07027
                                                                                                                                                                                                                                                                                                                                            09-FEB-1999 (first entry)
                                                                                                                                                                                                Ouery Match
Best Local Similarity 80.0
المالية 8
                                                                                                                                                                                                                                                                                                                                                                                                  prostate-specific antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tindall DJ,
                                                             Katz AE,
                                                                            WPI; 1995-373812/48.
N-PSDB; AAT04864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-594592/50.
                                                                                                                                                                                                                                                             185 CSGDSGGPLV 194
                                                                                                                                                                                                                                             CXGDSGGPXV 10
                                                                                                                                                                                       237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostate cancer
                          15-APR-1994;
        14-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                     W09846795-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1998
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                                                            Buttyan R,
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                           AAW83213;
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                                                                                                                                                                                                                                                                                          RESULT 7
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                        one cell containing hK2 in a sample which comprises at least 107 to 109 cells; and (b) detecting the presence of the amplified hK2 DNA. The method can be used for detecting, monitoring the progression of and pathologically staging prostate cancer. The present sequence represents prostate-specific antigen protein hK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             To detect both free and bound PSA, a second solid support with attached (differently labelled) monoclonal antibody binding free and bound PSA (especially selected from (c)) can be used either with, or in place of, the first solid support. The antibodies are useful in cancer screening, especially prostate and breast cancer. By obtaining total and free PSA values, their ratio can be used to separate prostatic cancer (PCa) from benign prostatic hyperplasia (BHP) patients. Measurement of PSA is also useful after radical prostatectomy, to predict disease persistence. The
oligonucleotides to amplify the DNA by PCR to yield amplified hK2 DNA, where the conditions amplify the DNA obtained by RT of RNA from at lea one cell containing hK2 in a sample which comprises at least 107 to 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specific antigen; PSA; epitope; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful, e.g. in screening for prostate or breast cancer and especially to distinguish between benign prostatic hyperplasia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents prostate specific antigen (PSA).
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 19;
Pred. No. 84;
); Mismatches 2;
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                  Homo saptens
                                                                                                                                                                                                                                              27-APR-1999
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                                                                                                                                                                                                            AAW96187;
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   antibodies allow evaluation of PSA free/total ratio, enabling separation of BPH and PCa patients with PSA values 4-10~\rm ng/ml not previously possible by total PSA testing, avoiding biopsies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This polypeptide comprises human prostate-specific antigen (PSA)

C hK3. PSA levels are widely used as a prognostic indicator of prostate carcinoma. The invention provides a novel diagnostic method comprising contacting antibodies that specifically bind to method comprising contacting antibodies that specifically bind to human prostate specific glandular kallikrein protein hK2 (see WA53950 or pro-hK2 (phK2, see AAW45396), but not with PSA, with a sample of physiological fluid from a human. The assay is based on the discovery that phK2 is detected in the supernatant of a prostate carcinoma cell line and that hK2 is present in human physiological fluid from prostate cancer cells. The method is useful for monitoring the treatment and/or progression of prostate cancer, or for the early detection of prostate cancer in males that have believed the cancer cells. The males that chave BPH or a high grade prostatic neoplasia (HPGN) or whose family members have or had BPH, HPGN or a prostate cancer. In males that
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   also be important in distinguishing between prostate cancer and BPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnostic methods using antibodies which bind prostate antigens useful for, e.g. monitoring treatment or progression of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    presence and/or amount of hK2 complexes with plasma proteins may
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saedi M, Tindall DJ;
                                                                                                  DB 19; Length 237;
84;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate-specific antigen; hK3; PSA; human; hK2;
prostate-specific glandular kallikrein; prostate carcinoma;
prostate cancer; benign prostatic hyperplasia; diagnosis.
                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Prostate-specific antigen protein hK3 (PSA).
                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 55-56; 100pp; English.
                                                                                                         Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grauer L, Klee GG, Mikolajczyk SD,
                                                                                                                                                                                                                                                                                                  AAW45398 standard; Protein; 237 AA.
                                                                                                         94.0%;
80.0%;
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                                                                                         Ouery Match
Best Local Similarity 80...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human kallikrein 2 (hK2) is expressed at elevated levels relative to
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of human kallikrein 2 - as a marker for developing products for the diagnosis, prognosis, monitoring and treatment of breast cancer
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                              Indels
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treatment; monitoring; prostate specific antigen; PSA.
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Pred. No. 84;
0; Mismatches
Pred. No. 84;
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate specific antigen (PSA).
                                                                                                                                                                                                                                                                         AAW96187 standard; Protein; 237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Young CYF;
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80.0%;
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(MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klee GG, Tindall DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monitoring hK2 levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-105632/09.
N-PSDB; AAX08947.
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Best Local Similarity
'-has 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TIND/) TINDALL D J. (YOUN/) YOUNG C Y F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 CSGDSGGPLV 194
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RESULT 11

DB 19; Length 237;

94.0%; Score 47;

Query Match

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Novel prostate specific antigen (PSA) for distinguishing benign prostatic hyperplasia from prostate cancer, comprises a clip at lysine 182 of the amino acid sequence of a mature form of PSA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a mature form of a novel form of prostate specific antigen (PSA). This form of PSA has at least 1 clip at Lys-182 and may additionally have 1 or more clips at Lys-1, Lys-145 and Lys-146. Preferably, the PSA contains at least 2 clips at Lys-145 and Lys-182. The novel forms of PSA exist at an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prostate specific antigen; PSA; BPSA; benign prostatic hyperplasia; BPH; marker; diagnosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prostate specific antigen specific to benign prostatic hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        elevated level in patients suspected of having benign prostatic hyperplasmia (BPH) and therefore may be used as a serum marker or an immunohistological marker to help distinguish BPH from prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer. Antibodies recognising the novel forms of PSA and immunoassays that detect and determine the novel forms of PSA are
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    /note- "site of internal peptide bond cleavage"
                                                /note= "site of internal peptide bond cleavage"
                                                                                               cleavage,
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                                                                                               "site of internal peptide bond
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Pred. No. 84;
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                                                                                                                                                                                                                                                                                                                               (HYBR-) HYBRITECH INC. (BAYU) BAYLOR COLLEGE MEDICINE.
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80.0%;
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182
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Best Local Similarity
'-has 8; Conserve
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                          Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel composition (A) having a total concentration of prostate-specific antigen (PSA). (A) is useful as a reference in methods for detecting PSA (a marker for prostatic cancer) in man blood or serum and to generate isoform-specific monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibodies (MAb) against PSA, for use in immunological assays. (A) contains all the isoforms of PSA and can be isolated without significant formation of artefacts by autoproteolysis. Antibodies specific for particular PSA isoforms can improve diagnostic specificity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition containing isoforms of prostate-specific antigen, useful a reference standard for analysis and for producing isoform-specific
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                                                                                                                                                                                                          Prostate-specific antigen; PSA; human; detection; prostatic cancer; isoform-specific monoclonal antibodies; marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prostate specific antigen elevated in benign prostatic hyperplasia.
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Pred. No. 84;
); Mismatches 2; Indels
                                                                                                                                                                Human prostate-specific antigen N-terminal fragment #2
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                     AAB11041 standard; peptide; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostate specific antigen; PSA; marker; immunoassay; diagnosis;
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80.0%;
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                                                                                                                  (first entry)
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185 CSGDSGGPLV 194
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jolk M, Mast W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Cleavage-site
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                                                                                                                  08-FEB-2001
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                                                                    AAB11041;
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AAB19818
AAB11041
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Gaps

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(first entry)
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N-PSDB; ABK86205.
                                                                                                                                                                                                                                                                     188 CSGDSGGPLV 197
                                                                                                                                                                                                                                             1 CXGDSGGPXV 10
                                                                                                                                                                      240 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200240059-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                          AAU98921;
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                                                                                                                                                                                                       Distinguishing prostate cancer from benign prostatic hyperplasia using different forms of prostate specific antigen contained in a sample involves mathematically combining amounts of ProPSA and BPSA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                              The present sequence represents a mature form of a novel form of prostate specific antigen (PSA). This form of PSA has at least 1 clip at Lys-182 and may additionally have 1 or more clips at Lys-14. Lys-145 and Lys-146. BPSA, a form of PSA that comprises at least 1 clip at Lys-182, exists at an elevated level in the transition zone of benign prostatic hyperplasmia (BPH) tissue, compared to peripheral zone cancer and non-cancer prostate tissues. A method for distinguishing prostate cancer from BPH involves determining the ratio of proPSA and BPSA in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen peptide derived from prostate specific antigen - does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSA; kallikrein; prostate cancer; antigenic; polyclonal antisera
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/note= "site of internal peptide bond cleavage"
                                                                                                                                                           Slawin K;
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                                                                                                                                                           Wolfert R,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 7
Pred. No. 84;
0; Mismatches
                                                                                                                                                           Rittenhouse H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnston DA, Kokolus WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW11023 standard; Protein; 240 AA.
                                                                                                                                                                                                                                                         Disclosure; Fig 14; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate specific antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                 94.0%;
80.0%;
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                                                                       12-APR-2000; 2000WO-US09789
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                           Wang T,
                                                                                                                       (HYBR-) HYBRITECH INC. (BAYU ) BAYLOR COLLEGE
                                                                                                                                                                                  WPI; 2001-007264/01.
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185 CSGDSGGPLV 194
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                                                                                                                                                         Mikolajczyk S,
                       WO200067030-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-0CT-1997
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                                                                                                30-APR-1999;
                                               09-NOV-2000
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Human; prostate specific antigen; PSA; cytostatic; antiviral; immunostimulant; cell-mediated immune response; tumour; breast cancer; virus infection; prostate cancer; colorectal cancer; pancreatic cancer; lymphoma; leukaemia; hepaduavirus; lentivirus; herpesvirus; human immunodeficiency virus; HIV; flavivirus; pestivirus.
                                                                                                                                                                                              which is used to produce novel peptides derived from the 240 residue sequence. The preferred peptides have two hydropholor regions and one hydrophilic region each of about 5 as in length, arranged as follows: hydropholic-hydrophilic-hydrophobic. Polyclonal antisera specific for the antigenic peptides may be used in a method for diagnosing prostate cancer in vivo or in vitro. The peptides represent a sequence unique to PSA which does not cross react with certain kallikreins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps.
                                                                                                                                                                   The present sequence represents human prostate specific antigen (PSA)
react with related kallikreins, for diagnosis of prostate
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/note This region is specifically claimed //note This region is specifically claimed //note This region is specifically claimed //note This region is specifically claimed
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/note= "This region is specifically claimed"
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Pred. No. 84;
0; Mismatches 2
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LOUK/) LOUKINOV D I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zoubak S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                  Claim 1; Fig 1; 74pp; English.
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80.0%;
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Best Local Similarity 80.00,
Best Local Similarity 80.00,
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Inducing a cell-mediated immune response against a target antigen, reducing undesired cells and stimulating presentation of an antigen by a cell, comprises administering a polynucleotide encoding a variant of an antigen

Claim 15; Page 122-123; 146pp; English.

The invention relates to a method of inducing a cell-mediated immune response against a cell comprising a target antigen (I) in a subject, treating a subject having undeasized cells, for example tumour cells cor virally infected cells (C). Treducing the number of (C) in a subject, and stimulating presentation of (I) by a cell. This is done by administering a polynucleotide (II) encoding a variant of (I), so that (II) expressed in a cell and cell-mediated immune response is induced. The method can be used to treat prostate cancer, breast cancer, colorectal cancer and pancreatic cancer, as well as lymphomas and colorectal cancer and pancreatic cancer, as well as lymphomas and infections such as those caused by hepadnaviruses, lentiviruses (including human immunodeficiency virus (HIV)), herpesviruses and the flaviviruses and pestiviruses. The present sequence represents the sequence deleted, used as a target antigen in the method of the

245 AA; Sequence

Gaps ö Query Match
Best Local Similarity 80.0%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 2; Indels

1 CXGDSGGPXV 10 à q

193 CSGDSGGPLV 202

Search completed: May 12, 2003, 15:36:03 Job time: 29.6 secs

OM protein

Run on:

Sequence:

Title:

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Sequence 2, Appli
Sequence 2, Appli
Patent No. 5352664
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Sequence 8, 8
Sequence 77,
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STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COMPUTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPY disk
COMPUTER: IBM PC COMPATABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/472,228A
FILING DATE: 07-JUN-195
CLASSIFICATION NUMBER: 37,642
ATTORNEY/AGRAT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSC:388
TELECOMMUNICATION INFORMATION:
TELEFONE (512) 418-3000
TELEFAX: --0424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Kokolus, William J.
APPLICANT: Fritsche, Herbert A.
APPLICANT: Fritsche, Herbert A.
APPLICANT: Tritsche, Dennis A.
TITLE OF INVENTION: IMMUNGENIC PEPTIDES OF PROSTATE
TITLE OF INVENTION: SPECIFIC ANTIGEN
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: ARIOId, White & Durkee
STREET: P.O. Box 4433
                                                                                                         US-08-381-088-2
US-08-330-594-8
US-08-48-455D-77
US-08-484-211C-77
US-08-906-769-77
US-08-906-769-77
US-08-906-7616-77
US-08-906-7616-77
US-08-906-78-77
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Pred. No. 0.12;
0; Mismatches
                            US-08-596-405-2
US-08-877-620-2
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                                                                                         5352664-3
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Best Local Similarity 80.0%;
Matches 8; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
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STRANDEDNESS:
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US-08-472-228A-19
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                                                                                                                                                                                                           May 12, 2003, 15:33:37; Search time 9.6 Seconds (without alignments) 30.649 Million cell updates/sec
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Sequence 19,
Sequence 11,
Sequence 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
                            GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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PCT-08-96-09303-19

US-08-844-024-2

US-08-718-547-2

US-08-718-547-2

US-08-718-547-2

US-08-76-825A-1

US-08-944-483-38

US-09-100-264-3

US-09-303-339-2

US-09-303-339-2

US-09-303-339-2

US-09-303-339-2

US-09-100-264-3

US-09-100-264-3

US-09-100-264-3

US-09-100-264-3

US-09-100-265-059-1

US-09-100-732-5

US-09-100-732-5

US-09-100-732-5

US-09-100-732-5

US-09-100-732-1

US-09-100-732-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                           US-09-909-348-2
50
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
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Minimum DB Maximum DB

Database

Result

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Searched:

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Pred. No. 1.1;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                             Length 20;
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibodies Specific for Human
Prostate Glandular Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Amino acid sequence of PSA (hK3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTORNEY/AGENT INFORMATION:
NAME: WGESSNEY, WARTEN D.
REGISTRATION NUMBER: 30,440
REFERENCE/OCKET NUMBER: 1016.62-US-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Merchant & Gould
3100 No. 5516639west Center
    APPLICATION NUMBER: PCT/US96/09303
                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,228
FILING DATE: 07-JUN-1995
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/096,946
FILING DATE: 19930722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08096946 Patent No. 5516639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 5540z
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPATIBLE IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                             20 amino acids
                                                                                                                                                                                                                                                                           Query Match 94.0
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minneapolis
                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                  ; TOPOLOGY: linear
PCT-US96-09303-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXGDSGGPXV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-096-946-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMUNOGENIC PEPTIDES OF PROSTATE SPECIFIC ANTIGEN
                                                                                                                                                                                                                IMMUNOGENIC PEPTIDES OF PROSTATE SPECIFIC ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                           ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,228
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                         United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application PC/TUS9609303
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                       APPLICANT: Fritsche, Herbert A. APPLICANT: Johnston Dennis A. TITLE OF INVENTION: IMMUNGENIC ITTLE OF INVENTION: SPECIFIC ANT NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                             Sequence 19, Application.US/09146831
Patent No. 6326471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.0%;
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-09-146-831-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
4 CSGDSGGPLV 13
                                                                                                                                                                                                                                                                                                                                  Houston
                                                                                                                                                                                                                                                                                                                                                      Texas
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CT-US96-09303-19
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Patent No. 6013471
GENERAL INFORMATION:
APPLICANT: Tindall, Donald J.
APPLICANT: Young, Charles Y.F.
APPLICANT: Saed1, Mohammed S.
TITLE OF INVENTION: DNA Encoding HK2 Variant Polypeptides
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lundberg, Woessner & Kluth, P.A
                                                                                                     SCETWARE: Patentin Release #1.0, Version #1.25
SCETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,547
FILING DATE: US/08/718,547
FILING DATE: US/08/718,547
FILING DATE: US/08/718,547
RAME: White, John P. REGISTRATION WUMBER: 28,678
RECISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 43677-A-PCT/JPW/MJG
TELEPHONICATION INFORMATION:
TELEPHONICATION INFORMATION:
TELEPHONICATION 1900-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/768,859A
FILING DATE: 17-DECEMBER-1995
                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08768859A
Patent No. 6013471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 237 amino acids TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,4
REFERENCE/DOCKET NUMBER:
                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman,
STREET: P.O. Box 2938
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-718-547-2
ZIP: 10036
MPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                     COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 185 CSGDSGGPLV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXGDSGGPXV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US.
ZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Minn
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-768-859A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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TITLE OF INVENTION: A Method For Molecular Staging Of NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 237;
                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Katz, Aaron E., et al.
TITLE OF INVENTION: A Method For Molecular Staging Of
TITLE OF INVENTION: Prostate Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/844,024
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,391
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Wilte, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4367
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEKX: (212) 647-6555
TELEKX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-718-547-2; Sequence 2, Application US/08718547; Patent No. 5976794; GENERAL INFORMATION:
                                                                                                                                 Sequence 2, Application US/08844024
Patent No. 5840494
                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-844-024-2
                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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STATE: New York
COUNTRY: U.S.A.
    185 CSGDSGGPLV 194
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                                                                                                               US-08-844-024-2
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NOVEL SERINE PROTEASE REAGENTS
AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                       Lundberg, Woessner & Kluth, P.A
                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
JURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,046B
FILLING DATE: 26-MARCH-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DAYA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: WOSSENEY, WARTEN D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 476,001US1
FELECHOUNICATION INFORMATION:
TELEPHONE: 612-373-6903
TELEPAX: 612-339-3061
                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: Abbott Laboratories
: 100 Abbott Park Road
Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLPITTS, TRACEY L. FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDWARD N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RUSSELL, JOHN C.
STEWART, KENT D.
STROUPE, STEVEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRANADOS, EDWAR
KLASS, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
--has 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                       SEE: Schwegman,
: P.O. Box 2938
Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 CSGDSGGPLV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXGDSGGPXV 10
                                                                                                                ZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-944-483-38
                                                                             STATE: 1
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                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Tindall, Donald J.
APPLICANT: Young, Charles Y.F.
APPLICANT: Saedi, Mohammed S.
TITLE OF INVENTION: DNA Encoding HK2 Variant Polypeptides
NUMBER OF SEQUENCES: 21
                                                                         Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                      ALDINESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A. STREET: P.O. Box 2938 CITY: Minneapolis STATE: MN
                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Saedi, Mohammed S.
APPLICANT: Mikolajczyk, Stephen D.
TITLE OF INVENTION: Stable Variant HK2 Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CORRELTATION NUMBER: US/08/767,820A
FILING DATE: 17-DECEMBER-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                Sequence 1, Application US/08767820A Patent No. 6093796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08622046B Patent No. 6103237 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 545.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
                                                                         94.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-768-859A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 CSGDSGGPLV 194
                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                     1 CXGDSGGPXV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55402
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US-08-767-820A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
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                                                                                                                                                                                                                     94.0%; Score 47; DB 4; Length 237; 80.0%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application PC/TUS9407329
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical
APPLICANT: Education and Research
TITLE OF INVENTION: Antibodies Specific for Human
TITLE OF INVENTION: Prostate Glandular Kallikrein
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZUETTE: 55402
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US94/07329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 5;
Pred. No. 1.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Amino acid sequence of PSA (hK3)
PCT-US94-07329-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schwegman, Lundberg & Woessner
                                                                                                                                                                                                                                                              0; Mismatches
                      APPLICATION NUMBER: US/09/303,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3500 IDS Center
80 South Eighth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: RABSCH, Kevin W.
REGISTATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.
TELEPHONE: 612-339-0331
                CURRENT APPLICATION NUMBER: US/U9-CURRENT FILING DATE: 1999-04-30 NUMBER OF SEQ ID NOS: 2 SOFFWARE: Patentin version 3.0 SEQ ID NO 2 LENGTH: 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 94.0%;
Best Local Similarity 80.0%;
Matches 8; Conservative
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Best Local Similarity 80.00,
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                     TYPE: PRT
CRGANISM: Homo sapiens
US-09-303-339-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 CSGDSGGPLV 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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Association with Prostate Tissues From Prostate Peripheral Zone
Zone
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Sequence 3, Application US/09100264

Sequence 3, Application US/09100264

Sequence 3, Application US/09100264

Sequence 3, Application US/09100264

GENERAL INFORMATION:

APPLICANT: Tindall, Donald J.

APPLICANT: Ries, George G.

TITLE OF INVENTION: Method for detection of breast cancer.

FILE REFERENCE: 545.006051

CURRENT APPLICATION NUMBER: US/09/100,264

CURRENT FILING DATE: 1998-06-19

EARLIER APPLICATION NUMBER: US 60/050,963

SALLIER FILING DATE: 1997-06-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 237
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Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Pred. No.
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; Patent No. 6423503
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mikolajczyk, Stephen
APPLICANT: Wang, Tang
APPLICANT: Harry, Rittenhouse
APPLICANT: Robert, Wolfert
                                                                                                  NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 616
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: No. 6232456e
US-08-944-483-38
                                                                                                                                                                                                                                                                                                                                                                                                                         94.08;
80.08;
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80.0%;
                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 80.v.
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 CSGDSGGPLV 194
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 3
LENGIH: 237
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB Pred. No. 1.1; 0; Mismatches
                                                 CURRERY APPLICATION DATA:
APPLICATION NUMBER: US/08/472,228A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORREY/AGENT INFORMATION:
NAME: H19hlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSC:388
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: May 12, 2003, 15:40:37 Job time: 11.6 secs
                                                                                                                                                                                                       : TELEFAX: (512) 418-3000
: TELEFAX: (512) 474-7577
TELEX: 79-0924
: INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TUBOTH: 240 aning
                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                      LENGTH: 240 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 94.0
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11near;
MOLECULE TYPE: protein
US-08-472-228A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |||||| |
188 CSGDSGGPLV 197
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Patent No. 5807978
GENERAL INFORMATIONS
APPLICANT: Fritsche, Herbert A.
APPLICANT: Johnston, Dennis A.
TILLE OF INVENTION: IMMUNOGENIC PEPTIDES OF PROSTATE
TITLE OF INVENTION: SPECIFIC ANTIGEN
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06157
                                                                                                                                                                                                                                             E: Schwegman, Lundberg & Woessner, P.A 3500 IDS Center
                                                                       Mayo Foundation for Medical Education and Research
                                                                                                            APPLICANT: Hybritech Incorporated
APPLICANT: Tindall, Donald J.
APPLICANT: Young, Charles Y.F.
APPLICANT: Saedi, Mohammed S.
TITLE OF INVENTION: Recombinant HK2 Polypeptide
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ed. No. 1.1
                                                                                                                                                                                                                                                                                                                  ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States of America
                               Sequence 1, Application PC/TUS9506157
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: REASENT INFORMATION:
NAME: STARTION NUMBER: 35,561
TELECOMOVICATION INFORMATION:
TELEPHONE: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
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80.0%;
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MEDIUM TYPE: Floppy disk
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amino acid
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-06157-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman
                                                                                                                                                                                                                                                                                Minneapolis
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COUNTRY: Unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                    STATE: M
COUNTRY:
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US-08-472-228A-1
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Query Match
Best Local Similarity
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                                                                                                         May 12, 2003, 15:38:52; Search time 19.4 Seconds (without alignments) 47.436 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, 8
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Sequence 1,
Sequence 11,
Sequence 6,
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Sequence 1
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Sequence 3
Sequence 2
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/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:
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pubpaa/US09_PUBCOMB.pep
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-183-992-8
US-09-895-793-947
US-09-822-827-947
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US-09-874-238-6
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA:
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                   Title:
Perfect score:
Sequence:
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Maximum DB
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10 US-09-909-348-2 10 US-09-909-122-1 10 US-09-909-122-2 9 US-10-050-511-2	9 US-10-125-459-18 9 US-10-125-459-19 9 US-10-067-761-33 10 US-10-067-761-34	10 US-09-904-090-2 10 US-09-904-090-4 10 US-09-804-156-33 10 US-09-804-156-34		0 US-09-882-41-6 1 US-09-826-290-247 9 US-10-045-170A-16 9 US-10-050-692-6 9 US-10-050-692-6	9 US-10-050-611-4 9 US-10-050-688-5
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ALIGNMENTS

IITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND IITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER NUMBER OF SEQ ID NOS: 982 SOFTWARE: FastSEQ for Windows Version 3.0 FILE REFERENCE: 210.121.534.2 CURRENT APPLICATION NUMBER: US/09/895,793 CURRENT FILING DATE: 2001-06-29 Houghton, Raymond L. Vinals de Bassols, Carlota Sequence 946, Application US/09895793 Publication No. US20020192763A1 Mitcham, Jennifer L. Harlocker, Susan L. Jiang, Yuqiu McNeill, Patricia D. enderson, Robert A Vedvick, Thomas S. Carter, Darrick Skeiky, Yasir A.W Hepler, William T Kalos, Michael D. Retter, Marc W. Stolk, John A. APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. Day, Craig H. Samuel X. TYPE: PRT CRGANISM: Homo sapiens US-09-895-793-946 ang, Aijun

Score 47; DB 9; Length 261; Pred. No. 1.3;

94.0%;

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Sequence 6, Application US/09963896
Patent No. US20020102585al
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
Gueglar, Karl J.
Corley, Neil C.
TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
                                                   Sequence 946, Application US/09822827

Batent No. US20020081680A1

GENERAL INFORMATION:

APPLICANT: XU, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C1

CURRENT APPLICANION NUMBER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0

SQUID NO 946
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 10; Length 261; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION TELEPHONE: (650) 855-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 26-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (650) 855-05
TELEFAX: (650) 845-4166
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80.0%;
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
US-09-822-827-946
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Best Local Similarity
Matches 8; Conserv
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                                                US-09-822-827-946
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US-09-963-896-6
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TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: and Regulating Anglogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
FRIOR APPLICATION NUMBER: US 09/413,049
PRIOR PILING DATE: 1999-10-06
PRIOR PILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 09/316,802
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US-09-796-294-10
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80.0%; Pred. No. 1.3;
Live 0; Mismatches 2; Indels
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    Indels
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APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: Extracellular Serine Protease
FILE REFERENCE: D6020CIP3
CURRENT APPLICATION UMBER: US/09/796, 294
CURRENT FILING DATE: 2001-02-28
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47;
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PRIOR FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 72
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PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR FILING DATE: 1998-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No
                                                                                                                                                                                                Sequence 62, Application US/10131241 Publication No. US20030012792A1 GENERAL INFORMATION:
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Patent No. US20020037581A1
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Best Local Similarity 80.0%;
Matches 8; Conservative
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 80.0°
Matches 8; Conservative
  Conservative
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US-10-131-241-62
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                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Jensenius, Jens Chr.
APPLICANT: Thiel, Steffer
TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND
TITLE OF INVENTION: USES FOR IT
FILE REFERENCE: 09011-002003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 10;
Pred. No. 3.3;
0; Mismatches 2;
                        Pred. No. 1.9;
0; Mismatches
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PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
PRIOR PLICATION NUMBER: 60/042,678
PRIOR FLILING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PASTERO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/874,238 CURRENT FILING DATE: 2001-06-04
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Pred. No.
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US-09-874-198-6
; Sequence 6, Application US/09874198
. Patent No. US20020082208A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09874238
Patent No. US20020082209A1
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                        80.08;
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
                     Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo saptens
US-09-874-198-6
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                                                                                                                                                                    323 CSGDSGGPLV 332
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US-09-874-238-6
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TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: and Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0343 43170-261379
CURRENT APPLICATION NUMBER: US/09/907,402
CURRENT APPLICATION NUMBER: US 09/907,602
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-06-21
PRIOR FILING DATE: 1999-06-31
PRIOR FILING DATE: 1999-06-31
PRIOR FILING DATE: 1999-06-31
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN VERSION 3.1
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Patent No. US20020099189A1
GENERAL INFORMATION:
TILLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
FILE REFERENCE: 2786-0156P
CURRENT APPLICATION NUMBER: US/09/755,100
CURRENT FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: IL 128587
PRIOR APPLICATION NUMBER: IL 129439
PRIOR PLING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: IL 129439
PRIOR PLLING DATE: 1999-04-14
PRIOR PELICATION NUMBER: IL 131363
PRIOR PLICATION NUMBER: IL 131363
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                                                                                                                                           DB 10; Length 261;
1.3;
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                                                                                                                                                                                                         0; Mismatches
; CLONE: 130989
; SEQUENCE DESCRIPTION: SEQ ID NO: 6 :
US-09-963-896-6
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Patent No. US20020137668A1
GENERAL INFORMATION:
APPLICANT: Holaday, John W.
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80.0%;
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80.0%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 375
                                                                                                                                                                          Best_Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-402-1
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209 CSGDSGGPLV 218
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Best Local Similarity
Matches 8; Conserv
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US-09-755-100-11
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US-09-907-402-1
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APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.53462
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT PILLING DATE: 2001-06-29
NUMBER OF SEQ 1D NOS: 982
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/10183992
Sequence 6, Application US/10183992
Publication No. US20030054432A1
Publication No. US20030054432A1
APPLICANT: Chen, Lin
APPLICANT: Pepe, Michael
TITLE OF INVENTION: Methods and Reagents for Detecting Endotoxin
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                                                                                                                                                               Coughton, Raymond L.
Inals de Bassols, Carlota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 947, Application US/09822827
Patent No. US20020081680A1
                                                                                        Repler, William T.
Henderson, Robert A
                                                                                                                                            McNeill, Patricia D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.0%;
80.0%;
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80.0%;
                                                                         keiky, Yasir A.W
                    Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 94.0
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                             John
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US-09-895-793-947
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                                                                                                                                                                                  Vinals
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US-09-822-827-947
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                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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TITLE OF INVENTION: Methods and Reagents for Detecting Endotoxin
FILE REPERBENCE: 02877.00008
CURRENT APPLICATION NUMBER: 2002-06-28
PRIOR APPLICATION NUMBER: US 60/310,125
PRIOR PILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                             APPLICANT: Chen, Lin
APPLICANT: Chen, Lin
APPLICANT: Pepe, Michael
TILLE OF INVENTION: Methods and Reagents for Detecting Endotoxin
FILE REFERENCE: 02877-00008
GURRENT APPLICATION NUMBER: US/10/183,992
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 60/310,125
PRIOR FILING DATE: 2001-06-28
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                                                                                                                                                                                                                                                                                                                                                     94.0%; Score 47; DB. 80.0%; Pred. No. 4.8; tive 0; Mismatches
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                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-183-992-8
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                Sequence 4, Application US/10183992
Publication No. US20030054432A1
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Publication No. US20030054432A1
GENERAL INFORMATION:
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US-10-183-992-4
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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80.0%;
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Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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Matches 8; Conservative
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962 CSGDSGGPLV 971
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                                                  GENERAL INFORMATION
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US-09-895-793-947
                                                                                                                                                                                                                                               SEQ ID NO 4
LENGTH: 1019
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US-10-183-992-4
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APPLICANT: Crowther, Roger S.
APPLICANT: Standing, Dariell H.
APPLICANT: Standing, David J.
APPLICANT: Standing, David J.
APPLICANT: Redin, William R.
TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
TITLE OF INVENTION: PEPTIDE DERIVATIVES
FILE REFERENCE: 3033.1002-004
CURRENT APPLICATION NUMBER: US/10/050,692
CURRENT APPLICATION NUMBER: 09/909,122
PRIOR APPLICATION NUMBER: 60/219,300
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
NUMBER OF SED ID NOS: 6
SOFTWARE: FESTSED for Windows Version 4.0
                                                                                                                                                                                                                                                                                               Score 47; DB 9; Length 1083; Pred. No. 5.1; 0; Mismatches 2; Indels
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Pred. No. 0.089;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: fragment of human prothrombin
US-10-050-692-1
FILE REFERENCE: 02877.00008
CURRENT APPLICATION NUMBER: US/10/183,992
CURRENT FILING DATE: 2002-066-28
FRIOR APPLICATION NUMBER: US 60/310,125
FRIOR FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 1083 ·
                                                                                                                                                                                                       : TYPE: PRT ; ORGANISM: Carcinoscorplus rotundicauda US-10-183-992-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-050-692-1
; Sequence 1, Application US/10050692
; Publication No. US20020182205Al
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 92.0%;
Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                               94.08;
80.08;
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Best Local Similarity 80.0
Matches 8; Conservative
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Search completed: May 12, 2003, 15:59:09 Job time: 20.4 secs

1 CEGDSGGPFV 10

g

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chymotrypsin-like proteinase (EC 3.4.21.-) precursor - california red abalone clymotrypsin-like proteinase (EC 3.4.21.-) precursor - california red abalone)
C; Species: Haliotis rufescens (California red abalone)
C; Date. (O'-Apr-1994 #sequence_revision 19-May-1994 #text_change 22-Jun-1999
C; Accession: 633585; 632750
R; Groppe, J.C.; Morse, D.E.
Arch. Bloothew. Blophys. 305, 159-169, 1993
A; Title: Molluscan chymotrypsin-like protease: structure, localization, and substrate A; Reference number: 635585; MUID: 93343624; PMID: 8342947
A; Recidues: 12-28 < GRODA
A; Residues: 1-234 < GRODA
A; Residues: 1-234 cGRODA
A; Cross-references: EMBL:X71438; NID: 9296361; PIDN: CAA50572.1; PID: 9296362
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; intestine; serine proteinase; zymogen
F; 1-237Domain: aignal sequence #status predicted <SIG>F; 23-254/Product: chymotrypsin-like proteinase #status predicted <MAT>F; 24-251/Domain: trypsin homology <TRY>F; 24-251/Domain: trypsin homology <TRYPSIN trypsin homology <TRYPSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-May-1997
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-May-1997
C;Accession: PG1235; PG1236
B;Title: Presence of a serine protease in the complement activating component of the A;Reference number: PG1235; MUD: 93176166; PMID: 8439319
A;Reference number: PG1235
A;Molecule type: mRNA
A;Recidues: 1-251 - TAK>
A;Accession: PG1236
A;Molecule type: protein
A;Recidues: 1-181,122-135;155-173;182-201 <TAZ>
C;Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement facto C;Reywords: hydrolase; serine proteinse
F;1-243/Domain: trypsin homology <TRV>
                                                                                                                                                                                                                                                                                                        trypsin (EC 3.4.21
chymotrypsin B - A
chymotrypsin (EC 3
chymotrypsin (EC 3
kallikrein-like se.
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trypsin (EC 3.4.21
tryptase (EC 3. tryptase (EC 3. trypsin (EC 3. thrombin (EC 3. trypsin (EC 3. try
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llarity 80.0%; Pred. No. 0.36;
Conservative 0; Mismatches 2; Indels
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Pred. No. C
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                                                                         S31779
G42696
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ilarity 80.0%;
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                                                                                                                                                                                                                                                                               (without alignments)
84.328 Million cell updates/sec
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                                                                                                                                                                                                                                                May 12, 2003, 15:33:02; Search time 11.4 Seconds
                                         GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283224 segs, 96134422 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Cross-references: EMBL:017040; NID:9595945; PIDN:AAA56764.1; PID:9595946
Monne, M.; Croce, C.M.; Yu, H.; Diamandis, E.P.
ancer Res. 54, 6344-6347, 1994
Title: Molecular characterization of prostate-specific antigen messenger RNA expres
Reference number: 152712; MUID:95079406; PMID:7527295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 5-210, WVILITELIMPA',223,'PMVLHGSLV',233,'WRGGV' <R13>
A;Cross-references: GB:M21896; NID:g189525; PIDN:AAA59996.1; PID:g189526
A;Note: the authors translated the codon GGC for residue 28 as Arg and TGG for residu
A;Accession: B31567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M21895; NID:q189523; PIDN:AAAS9995.1; PID:q189524
A;Note: the authors translated the codon GGC for residue 28 as Arg and TGG for residu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Blochem. 220, 45-53, 1994
A;Title: Complex formation between protein C inhibitor and prostate-specific antigen A; Reference number: S41212; MUID:94164172; PMID:7509746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Reaidues: 25-261 <SC2>
R; Watt, K.W.K.; Lee, P.J.; M'Timkulu, T.; Chan, W.P.; Loor, R.
Proc. Natl. Acad. Sci. U.S.A. 83, 3166-3170, 1986
A; Title: Human prostate-specific antigen: structural and functional similarity with A; Reference number: A23937; MUID:86205857; PMID:2422647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 5-164, CTPGPDGAAGSPDAWV' <R14>
A; CTOSS-references: GB:MAIB97; NID:9189529; PIDN:AAAS9997.1; PID:9189530
A; Note: the authors translated the codon GGC for residue 28 as Arg, TGG for residue R; Schaller, J: Akiyama, K:; Fauda, R:; Hara, M:; Marti, T:; Rickli, E.E.
Eur. J Biochem. 170, 111-120, 1987
A; Title: Isolation, characterization and amino-acid sequence of gamma-seminoprotein, A; Reference number: S00212; MUID:880082806; PMID:3691515
                                                                                                                                                    A;Residues: 5-261 <LU2>
R;Riegman, P.H.J.; Klaassen, P.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, Blochem. Blophys. Res. Commun. 155, 181-188, 1988
A;Title: Molecular cloning and characterization of novel prostate antigen cDNA's. A;Reference number: A90144; MUID:88326297; PMID:2458104
A;Accession: C31567
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A;Residues: 'PQAYHLHPESCVT',1-176 <RES>
A;Cross-references: GB:S75755; NID:g861469; PIDN:AAD14185.1; PID:g4261885
R;Christensson, A.; Lilja, H.
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A; Residues: 25-93, 'T', 95-164, 'HL', 166, 'YDQM', 169-174, 'Q', 176-261 <WAT>
R; Moreno, J.M.
submitted to the EMBL Data Library, November 1994
A; Reference number: G07735
A; Accession: G01551
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:Residues: 25-30,'X',32-49 <CHR>
:Comment: This enzyme preferentially cleaves after tyrosine residues.
A; Reference number: A26757; MUID:87190978; PMID:2436946
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A; Introns: 16/1; 69/2; 165/1; 210/3
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin prostate; seri
E; 11/7/Domain: signal sequence #status predicted < F; 18-24/Domain: propeptide #status predicted < PRO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 5-261 <RI2>
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                                                                                                         A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S00232
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D1gby, M.; Zhang, X.Y.; Richards, R.I.
Cleic Acids Res. 17, 2137, 1989
Title: Human prostate specific antigen (PSA) gene: structure and linkage to the kallik
Reference number: $03604; MUID:89183632; PMID:2467258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A31
                                                                                                                                                                                                                                                                                                                                                                                       semenogelase (EC 3.4.21.77) precursor (validated) - human
N;Alternate names: gamma-seminoprotein; P-30 antigen; prostate-specific antigen; prostat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Homo sapiens (man) properties of the species of the speci
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cochem. Blophys. Res. Commun. 160, 903-910, 1989
Title: CDNA coding for the entire human prostate specific antigen shows high homologie
Reference number: A32546; MUID:89246551; PMID:2470373
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Nucleic Acids Res. 16, 6226, 1988
A;Title: Sequence of a cDNA clone encompassing the complete mature human prostate specif
A;Reference number: S02239; MUID:88289366; PMID:2456523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ochem. Biophys. Res. Commun. 161, 1151-1159, 1989
Title: Characterization of the gene for prostate-specific antigen, a human glandular
Reference number: A32423; MUID:89302090; PMID:2472789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
Residues: 1-72,'T',74-85,'I',87-174,'P',176-183,'Q',185-259,'D',261 <HEN>
Cross-references: GB:M26663
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itle: Genomic sequence of human prostate specific antigen (PSA).
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Klobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler,
Dmitted to the EMBL Data Library, May 1989
Reference number: S05468
Accession: S05468
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Cross-references: EMBL:X07730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residues: 1-261 <RIE>
Cross-references: GB:M24543
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FEBS Lett. 214, 317-322, 1987
                                                                                                         CSGDSGGPLV 217
                                               1 CXGDSGGPXV 10
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lesidues: 1-261 <LUN>
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esidues: 1-261 <DIG>
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lesidues: 1-261 <KL1>
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Residues: 1-29 <KL2>
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Residues: 17-63,'T',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tatus: preliminary
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Cyclear CDB:MASP1; GDB:CRARF; CRARF1; PRSS5; MASP
A;Cross-references: GDB:361104; GDB:330954; OMIM:600521
A;Cross-references: GDB:361104; GDB:330954; OMIM:600521
C;Map position: 3427-348
C;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement facto
C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; hy
F;1-17/Donain: signal sequence statutus predicted <SIG>
F;18-448 449-699/Product: Ra-reactive factor #status predicted <MAT>
F;18-135/Domain: Clr/Cls repeat homology <CIR1>
F;19-135/Domain: Clr/Cls repeat homology <CIR2>
F;301-362/Domain: Complement factor H repeat homology <FH1>
F;307-320/Domain: complement factor H repeat homology <FH2>
F;449-691/Domain: trypsin homology <RRY>
F;449-178,407/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;391/143-157,153-166,168-181,185-212,242-260,301-349,329-362,367-414,397-432,436-5
F;499,552,646/Active site: Arg-Ile (autolytic) #status predicted
F;490,552,646/Active site: His, Asp, Ser #status predicted
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NyAlternate names: coagulation-complement factor C; Limulus factor C interactions: coagulation factor C heavy chain; coagulation factor C light chain peptid C; Species: Tachypleus tridentatus
C; Species: Tachypleus tridentatus
C; Accession: A38738; B38738; B38738; B38738; B38738; B7878; B78788; B78788; B78788; B78788; B78788; B78788; B78788; B78788; B78788; B78
                                                              R;Takada, F.; Takayama, Y.; Hatsuse, H.; Kawakami, M.
Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A;Title: A new member of the Cls family of complement proteins found in a bactericida
A;Reference number: JNO883; MUID:94059062; PMID:8240317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-234, E',236-284, G',286-498, K',500-542, K',544-642, S',644-699 <TAK>
A;Cross-references: DDBJ:D17525; NID:g439712; PIDN:BAA04477.1; PID:g439713
A;Experimental source: liver
C;Comment: This is a serum bactericidal factor that activates complement C4 and C2
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A;Residues: 1-1019 <MUT>
A;Cross-references: GB:D90271; NID:g217396; PID:d1015020; PID:g217397
A;Accession: B38738
A;Accession: B38738
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Pred. No. 0.92;
0; Mismatches 2; Indels
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A; Molecule type: mRNA
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80.0%;
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Matches 8; Conserv
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A; Residues: 1-699 <SAT>
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NiAlternate names: TESP2
C; Species: Mus musculus (house mouse)
C; Date: 2.2-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C; Accession: JE0105
R; Kohno, N.; Yamagata, K.; Yamada, S.; Kashiwabara, S.; Sakai, Y.; Baba, T.
Blochen: Biophys: Res. Commun. 245, 658-665, 1998
A; Title: Two novel testicular serine proteases, TESP1 and TESP2, are present in the mous A; Accession: JE0104; MUID: 98249770; PMID: 9588171
A; Molecule type: mRNA
A; Mesidues: 1366 CKOH>
A; McCassion: Je060>
A; Cross: references: DDBJ:AB008911: NTD: 2007770;
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C;Comment: This protein is localized in the sperm acrosome and is released during the ac
C;Superfamily: trypsin homology
C;ReyWords: hydrolase; serine proteinase
F;71-310/Domain: trypsin homology <TRX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Semenogelase (EC 3.4.21.77) precursor - rhesus macaque
N;Alternate names: gamma-seminoprotein; P-30 antigen; prostate-specific antigen; prostate
C;Species: Macaca mulatta (rhesus macaque)
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
C;Accession: S35711; S34239
R;Gauthier, E.R.; Chapdelaine, P.; Tremblay, R.R.; Dube, J.Y.
A;Title: Characterization of rhesus monkey prostate specific antigen cDNA.
A;Reference number: S35711; MUID:9336542; PMID:7689340
A;Accession: S35711
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A; Residues: 1-261 <GAU>
A; Residues: 1-261 <GAU>
A; Cross-references: EMBL:X73560; NID:g311843; PIDN:CAA51957.1; PID:g311844
C; Comment: This enzyme preferentially cleaves after tyrosine residues.
C; Superfamily: trypsin; trypsin homology serine proteinase
C; Reywords: glycoprotein; hydrolase; prostate; serine proteinase
F; 1-17/Domain: signal sequence *status predicted <SIG>
F; 18-24/Domain: stopeptide *status predicted <PRO>
F; 25-261/Product: semenoglase *status predicted <MAT>
F; 25-253/Domain: trypsin homology <TRY>
F; 55, 120, 213/Active site: His, Asp, Ser *status predicted
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80.0%; Pred. No. 0.36;
ive 0; Mismatches 2; Indels
                                                                              Length 261;
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F;65,120,213/Active site: His, Asp, Ser #status predicted
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Pred. No. 0.5;
0; Mismatches
                                                                              DB 1;
                                                                                                                   0.36;
                                                                          Score 47; DB 1
Pred. No. 0.36;
0; Mismatches
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                          Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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262 CAGDSGGPLV 271
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chymotrypsin-like proteinase (EC 3.4.21..) - pig (tentative sequence) (fragments) chymotrypsin-like proteinase (EC 3.4.21..) - pig (tentative sequence) (fragments) N.Alternate names: pancreatic elastase II [misidentification] C;Species: Sus scrofa domestica (domestic pig) C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000 C;Accession: A23473
E;Vered, M.; Gertler, A.; Burstein, Y.
Int. J. Pept. Protein Res. 27, 183-190, 1986
A;Reference number: A23473; MUID:86194934; PMID:3634756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elastase (EC 3.4.21.-) 2B - horse (fragments)
C;Species: Equus caballus (domestic horse)
C;Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 07-May-1999
     02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
                                                                                                                                                                                   A)Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule-type: mRNA
A;Residues: 1-66 CRES.
A;Residues: 1-66 CRES.
A;Cress-references: GB:K01654; NID:g198490; PIDN:AAA39346.1; PID:g198491
C;Superfamily: trypsin; trypsin homology
F;1-58/Domain: trypsin homology (fragment) <TRX>
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R)Dubin, A.; Potempa, J.; Travis, J.
Blochem. J. 300, 401-406, 1994
A;Title: Structural and functional characterization of eA;Reference number: S44461; MUID:94271153; PMID:7516152
                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 2;
Pred. No. 0.15;
1; Mismatches
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A; Residues: 1.31; 32-56; 57-73 < DUB>
C; Superfamily: trypsin; trypsin homology
C; Reywords: hydrolase; serine proteinase
F; 1-73/Domain: trypsin homology (fragments) < TRY>
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Pred. No.
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70.0%;
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Best Local Similarity
7; Conserve
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A;Molecule type: protein
A;Residues: 1-126 <VER>
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Matches 8; Conserv
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14 CAGDSGGPLI 23
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                                                                                                                                                                                                       Wolecule type: protein '17',43-54,'E';691-782;950-977 crock>
standard type: protein factor C; C-type lectin homology; complement factor H repeat
'Skandues' 'S',73-79, 'S',41,'T',43-54,'E';691-782;950-977 complement factor C; C-type lectin homology; complement factor H repeat
'Keywords: alternative splicing; glycoprotein; hemolymph coagulation; hydrolase; serine
'1-25/Domain: coagulation factor C heavy chain #status experimental cf 690/Product: coagulation factor C heavy chain #status experimental cf 7:136-195/Domain: complement factor H repeat homology cf 195/Domain: complement factor H repeat homology cf 196/Domain: complement factor H repeat homology 
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11. Cell. Biol. 9, 692-700, 1989
11itle: Levels of RNA from a family of putative serine protease genes are reduced in Dr
Reference number: JSO260; MUID:89219063; PMID:2469005
Accession: PSO049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :Tokunaga, F.; Miyata, T.; Nakamura, T.; Morita, T.; Kuma, K.I.; Miyata, T.; Iwanaga,
1r. J. Biochem. 167, 405-416, 1987
                                                                                   Eur. J. Blochem. 167, 405-416, 1987
A:Title: Lipopolysaccharide-sensitive serine-protease zymogen (factor C) of horseshoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - fruit fly (Drosophila melanogaster) (fragment)
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6-634/Domain: complement factor H repeat homology <PH04>
5-747/Domain: complement factor H repeat homology *status atypical <FH05>
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Date: 07-Jun-1990 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
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A;Experimental source: strain dnc mutant
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                                                                                                                                  s a novel type of serine protease.
Reference number: S00105; MUID:88004461; PMID:3308457
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F:1-53/Domain: trypsin homology (fragment) <TRY>
F:30/Binding site: substrate (Val) #status predicted
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Pred. No. 1.3;
0; Mismatches
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1-466,616,'DN',619-620,'A',622 <MU2>
erences: GB:D90272
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A;Map position: 3 99C-D
C;Superfamily: trypsin; trypsin homology
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C; Species: Mus musculus (house mouse)
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                  A; Molecule type: DNA
A; Residues: 1-161 <RES>
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Job time: 11.4 secs
A; Accession: I48158
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R;Murakawa; M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Bur. J. Haemiatol. 52, 162-168, 1994
A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of A;Title: umber: 146196; MUD:94222160; PMID:8168596
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(S.Uperfanailly: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Reywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F;1-161/Domain: trypsin homology (fragment) - TRRY>
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                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:V00828; GB:J00389; NID:952773; PIDN:CAA24211.1; PID:91334112
A; Experimental source: Quakenbush inbred strain
C; Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release
                                                                                                                             C; Species: Mus musculus (house mouse)
C; Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 16-Jun-2000
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 16-Jun-2000
E; Accession: A00939
E; Aistohards, R.I.; Catanzaro, D.F.; Mason, A.J.; Morris, B.J.; Baxter, J.D.; Shine, J. J. B.J. Chem. 257, 2758-2761, 1982
A; Title: Mouse glandular kallikrein genes. Nucleotide sequence of cloned cDNA coding fA; Accession: A00939; MUID:82142394; PMID:6174512
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul_1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coagulation factor Xa (EC 3.4.21.6) - rhesus macaque (fragment)
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; saliva; serine proteinase; submandibular gland
F;1-141/Domain: trypsin homology (fragment) <TRY>
F;8-101/Active site: Asp, Ser #status predicted
F;8-101,72-86,97-122/Disulfide bonds: #status predicted
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Pred. No. 0.35;
0; Mismatches 2; Indels
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                                                                                                      glandular kallikrein; kininogenin
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                                                                             kallikrein (EC 3.4.21.35), submandibular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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97 CAGDSGGPLI 106
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                                                                                                            N; Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 7
                                                                                                                                                                                                                                                                                                                                                A; Molecule type
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Best Local
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Gaps

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Length 191; Indels

DB 2;

0.41;

0; Mismatches Score 46; Pred. No. 0

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A;Cross-references: GB:D21216; NID:g415304; PIDN:BAA04757.1; PID:g455393
C;Superfamily: coggulation factor x; EGF homology; Gla domain homology; trypsin homology: C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglu F:1-161/Domain: trypsin homology (fragment) <TRYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (C;Superfamily: trypsin; trypsin homology C;Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement factor D (EC 3.4.21.46) - plg (fragment)
C.Species: Sus scrofa domestica (domestic pig)
C.Species: Sus scrofa domestica (domestic pig)
C.Species: Os Jul-1995 #sequence_revision 21-Jul-1995 #text_change 19-May-2000
C.Accession: S54115
R.Nicolas, N.
Submitted to the EMBL Data Library, April 1995
A.Recernce number: S54115
A.Recernce number: S54115
A.Status: preliminary
A.Molecule type: mRNA
A.Coross-references: EMBL: Z49058; NID: 9773264; PIDN: CAAB8844.1; PID: 9773265
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Pred. No. 0.35;
A; Status: preliminary; translated from GB/EMBL/DDBJ
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80.0%;
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Best Local Similarity Bu.v.
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GenCore version 5.1.4_p5_4578

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OM protein - protein search, using sw model

Run on: May 12, 2003, 15:32:07; Search time 5.8 Seconds
(without alignments)
71.511 Million cell updates/sec
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Title: · US-09-909-348-2
Perfect score: 50
Sequence: 1 CXGDSGGPXV 10

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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TRYI_DROME	CTRL_HALRU	KLK3_HUMAN	KLK3_MACMU	CRAR_HUMAN	CRAR_MOUSE	LFC_CARRO	LFC_TACTR	EL2B_HORSE	PRTC_CANFA	PRTC_CAPHI	PRTC_FELCA	PRTC_HORSE	PRTC_MACMU	TRY3_LUCCU	CTR2_VESOR	CTR2_VESCR	TRYP_SACER	TRYP_SQUAC	TRY2_SALSA	TRYP_PIG	TRYD_HUMAN	TRY3_SALSA	TRY5_AEDAE	TRY1_GADMO	TRYX_GADMO	TRY1_SALSA	TRY1_BOVIN	TRY1_XENLA	KLK6_HUMAN	TRY2_XENLA	CTRA_BOVIN	CTRB_BOVIN	
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1 KLK3_HADMAN P07289 hallot 24.0 1019 1 CRAR_HUMAN P08604 macaca 24.0 1019 1 LFC_TARTRO 026422 carcin at 22.0 157 1 PRTC_CANFA 028278 canis 46 92.0 157 1 PRTC_CANFA 028215 capis 46 92.0 157 1 PRTC_CAPH 028315 capis 46 92.0 157 1 PRTC_MACMU 028315 capis 46 92.0 157 1 PRTC_MACMU 028506 macaca 46 92.0 216 1 CTR2_VESCR 028315 capis 92.0 165 1 TRY3_LUCCU 028506 macaca 46 92.0 227 1 TRY2_SACER 028315 capis 92.0 227 1 TRY2_SACER 028315 capis 692.0 227 1 TRY2_SACER 029315 salmo 84 92.0 238 1 TRY2_ABDAR 09533 salmo 84 92.0 238 1 TRY2_ABDAR 091014 gadus 46 92.0 238 1 TRY3_ABDAR 091014 gadus 46 92.0 241 1 TRY2_AADMO 091041 gadus 46 92.0 241 1 TRY2_AADMO 091041 gadus 46 92.0 241 1 TRY2_AADMO 091041 gadus 82 92.0 241 1 TRY2_AADMO 091041 gadus 82 92.0 241 1 TRY2_SALSA 091041 gadus 92.0 241 1 TRY2_SAL	47 94.0 252 1 TRYL_DROME P55905 47 94.0 254 1 CTRL_HALRU P95003 47 94.0 261 1 KLK3_HUMAN P48740 47 94.0 261 1 KLK3_HUMAN P48740 47 94.0 1019 1 LFC_CARRO P48740 47 94.0 1019 1 LFC_CARRO P68175 46 92.0 157 1 PRTC_CAPH P78175 46 92.0 157 1 PRTC_CAPH Q28178 46 92.0 157 1 PRTC_MACMU Q2818 46 92.0 157 1 PRTC_MACMU Q2818 46 92.0 161 1 PRTC_MACMU Q2818 46 92.0 167 1 PRTC_MACMU Q2818 46 92.0 167 1 PRTC_MACMU Q28165 46 92.0 <t< td=""><td>47 94.0 252 1 TRYI_DROME P52905 47 94.0 254 1 CTRL_HALRU P07288 47 94.0 261 1 KLK3_MACMU P07288 47 94.0 261 1 KLK3_MACMU P943619 47 94.0 261 1 KLK3_MACMU P943619 47 94.0 1019 1 LFC_TACTR P98064 47 94.0 1019 1 LFC_TACTR P28064 46 92.0 157 1 PRTC_TACTR P28758 46 92.0 157 1 PRTC_TACTR P78358 46 92.0 157 1 PRTC_TACTR P783504 46 92.0 157 1 PRTC_MACMU P93604 46 92.0 161 1 PRTC_MACMU P93604 46 92.0 216 1 TRYI_LOCU P93604 46 92.0 218 1 CTR2_VESCR P00769 46 92.0 231 1 TRYI_SALSA P93604 46 92.0 241 1 TRYI_SALSA P93604</td><td>47 94.0 252 1 TRYL_DROME P52905 47 94.0 254 1 CTRL_HALRU P95003 47 94.0 261 1 KLK3_HACMU P9401 47 94.0 699 1 CRAR_HOUSE P86064 47 94.0 1019 1 LFC_CARRO P86064 47 94.0 1019 1 LFC_TACTR P86064 46 92.0 157 1 PRTC_CAPHI Q28115 46 92.0 157 1 PRTC_MACMI Q28116 46 92.0 161 1 PRTC_MACMI PRTC_MACMI 46 92.0 165 1 TRY2_ARCR PRTC_MACMI 46 92.0<td>47 94.0 254 1 CTRL_HALRU P55205 47 94.0 254 1 CTRL_HALRU P95203 47 94.0 261 1 KLK3_HUMAN P48740 47 94.0 261 1 KLK3_HUMAN P48740 47 94.0 1019 1 LFC_TARCH P48740 47 94.0 1019 1 LFC_TARCH P588175 46 92.0 157 1 PRTC_CAPHT P788175 46 92.0 157 1 PRTC_CAPHT Q28218 46 92.0 157 1 PRTC_CAPHT Q28316 46 92.0 157 1 PRTC_CAPHT Q28316 46 92.0 157 1 PRTC_CAPHT Q28316 46 92.0 161 1 PRTC_APCA Q28316 46 92.0 165 1 TRY2_ARCAR P70076 46 92.0</td><td>47 94.0 252 1 TRYI_DROME P52905 47 94.0 254 1 CTRL_HALNU P07288 47 94.0 261 1 KLK3_MACMU P07288 47 94.0 261 1 KLK3_MACMU P07288 47 94.0 261 1 KLK3_MACMU P07288 47 94.0 1019 1 LFC_TACTR P0708 P22.0 1019 1 LFC_TACTR P22.0 26278 P22.0 157 1 PRTC_PELCA P022.0 161 1 PRTC_PELCA P022.0 161 1 PRTC_PECCA P022.0 162 1 PRTC_PECCA P022.0 163 1 PRTC_PECCA P022.0 163 1 PRTC_PECCA P022.0 164 92.0 165 1 TRYI_LOCCU P03304 P0769 P02.0 229 1 TRYI_LOCCU P03304 P02.0 229 1 TRYI_LOCCU P022.0 P022.0 231 1 TRYI_SACAR P022.0 231 1 TRYI_SACAR P022.0 231 1 TRYI_SACAR P022.0 231 1 TRYI_SACAR P022.0 231 1 TRYI_LOCCU P03303 P022.0 241 1 TRYI_LOCCU P022.0 P022.0 241 1 TRYI_LOCCU P022.0 P022.0 241 1 TRYI_LOCCU P022.0 P022.0 241 1 TRYI_ROVIN P022.0 P022.0 244 1 TRYI_ROVIN P022.0 P022.0 245 1 TRYI_ROVIN P022.0 P0</td><td>47 94.0 254 1 TRYL_BROME P52905 47 94.0 254 1 CTRL_HALRU P07288 47 94.0 261 1 KIK3_MACMU P07288 47 94.0 261 1 KIK3_MACMU P48740 47 94.0 1019 1 LFC_TACTR P48740 47 94.0 1019 1 LFC_TACTR P20864 46 92.0 157 1 PRTC_TACTR P28175 46 92.0</td></td></t<>	47 94.0 252 1 TRYI_DROME P52905 47 94.0 254 1 CTRL_HALRU P07288 47 94.0 261 1 KLK3_MACMU P07288 47 94.0 261 1 KLK3_MACMU P943619 47 94.0 261 1 KLK3_MACMU P943619 47 94.0 1019 1 LFC_TACTR P98064 47 94.0 1019 1 LFC_TACTR P28064 46 92.0 157 1 PRTC_TACTR P28758 46 92.0 157 1 PRTC_TACTR P78358 46 92.0 157 1 PRTC_TACTR P783504 46 92.0 157 1 PRTC_MACMU P93604 46 92.0 161 1 PRTC_MACMU P93604 46 92.0 216 1 TRYI_LOCU P93604 46 92.0 218 1 CTR2_VESCR P00769 46 92.0 231 1 TRYI_SALSA P93604 46 92.0 241 1 TRYI_SALSA P93604	47 94.0 252 1 TRYL_DROME P52905 47 94.0 254 1 CTRL_HALRU P95003 47 94.0 261 1 KLK3_HACMU P9401 47 94.0 699 1 CRAR_HOUSE P86064 47 94.0 1019 1 LFC_CARRO P86064 47 94.0 1019 1 LFC_TACTR P86064 46 92.0 157 1 PRTC_CAPHI Q28115 46 92.0 157 1 PRTC_MACMI Q28116 46 92.0 161 1 PRTC_MACMI PRTC_MACMI 46 92.0 165 1 TRY2_ARCR PRTC_MACMI 46 92.0 <td>47 94.0 254 1 CTRL_HALRU P55205 47 94.0 254 1 CTRL_HALRU P95203 47 94.0 261 1 KLK3_HUMAN P48740 47 94.0 261 1 KLK3_HUMAN P48740 47 94.0 1019 1 LFC_TARCH P48740 47 94.0 1019 1 LFC_TARCH P588175 46 92.0 157 1 PRTC_CAPHT P788175 46 92.0 157 1 PRTC_CAPHT Q28218 46 92.0 157 1 PRTC_CAPHT Q28316 46 92.0 157 1 PRTC_CAPHT Q28316 46 92.0 157 1 PRTC_CAPHT Q28316 46 92.0 161 1 PRTC_APCA Q28316 46 92.0 165 1 TRY2_ARCAR P70076 46 92.0</td> <td>47 94.0 252 1 TRYI_DROME P52905 47 94.0 254 1 CTRL_HALNU P07288 47 94.0 261 1 KLK3_MACMU P07288 47 94.0 261 1 KLK3_MACMU P07288 47 94.0 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94.0 261 1 KLK3_HUMAN P48740 47 94.0 1019 1 LFC_TARCH P48740 47 94.0 1019 1 LFC_TARCH P588175 46 92.0 157 1 PRTC_CAPHT P788175 46 92.0 157 1 PRTC_CAPHT Q28218 46 92.0 157 1 PRTC_CAPHT Q28316 46 92.0 157 1 PRTC_CAPHT Q28316 46 92.0 157 1 PRTC_CAPHT Q28316 46 92.0 161 1 PRTC_APCA Q28316 46 92.0 165 1 TRY2_ARCAR P70076 46 92.0	47 94.0 252 1 TRYI_DROME P52905 47 94.0 254 1 CTRL_HALNU P07288 47 94.0 261 1 KLK3_MACMU P07288 47 94.0 261 1 KLK3_MACMU P07288 47 94.0 261 1 KLK3_MACMU P07288 47 94.0 1019 1 LFC_TACTR P0708 P22.0 1019 1 LFC_TACTR P22.0 26278 P22.0 157 1 PRTC_PELCA P022.0 161 1 PRTC_PELCA P022.0 161 1 PRTC_PECCA P022.0 162 1 PRTC_PECCA P022.0 163 1 PRTC_PECCA P022.0 163 1 PRTC_PECCA P022.0 164 92.0 165 1 TRYI_LOCCU P03304 P0769 P02.0 229 1 TRYI_LOCCU P03304 P02.0 229 1 TRYI_LOCCU P022.0 P022.0 231 1 TRYI_SACAR P022.0 231 1 TRYI_SACAR P022.0 231 1 TRYI_SACAR P022.0 231 1 TRYI_SACAR P022.0 231 1 TRYI_LOCCU P03303 P022.0 241 1 TRYI_LOCCU P022.0 P022.0 241 1 TRYI_LOCCU P022.0 P022.0 241 1 TRYI_LOCCU P022.0 P022.0 241 1 TRYI_ROVIN P022.0 P022.0 244 1 TRYI_ROVIN P022.0 P022.0 245 1 TRYI_ROVIN P022.0 P0	47 94.0 254 1 TRYL_BROME P52905 47 94.0 254 1 CTRL_HALRU P07288 47 94.0 261 1 KIK3_MACMU P07288 47 94.0 261 1 KIK3_MACMU P48740 47 94.0 1019 1 LFC_TACTR P48740 47 94.0 1019 1 LFC_TACTR P20864 46 92.0 157 1 PRTC_TACTR P28175 46 92.0

P80646 gadus morhu	P43983 Nelogerma n P06871 canis famil	P00762 rattus norv	P07146 mus musculu	P00763 rattus norv	P07477 homo sapien	P06872 canis famil	P07478 homo sapien	PO8426 rattus norv	P12788 rattus norv	Q9ukrO homo sapien
CTRB_GADMO	GILA_HELHO TRY1_CANFA	TRY1_RAT	TRY2_MOUSE	TRY2_RAT	TRY1_HUMAN	TRY2_CANFA	TRY2_HUMAN	TRY3_RAT	TRY4_RAT	KLKC_HUMAN
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245	240 246	246	246	246	247	247	247	247	247	248
92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0
4.6	4 4 0 4	46	46	46	46	46	46	46	46	46
34	ი 9 შ	37	38	39	40	41	42	43	44	45

ALIGNMENTS

cea; Hexapoda; Brachycera;	e J.D., 11e R.F., erson S.N.,	eiffer B.D., ilklog G.L.G., Baldwin D., asley E.M., akvov S., crandra I., s. P., chandra I., s. P.C., letz S.M., etz S.M., letschmann W., isser K.,	wam C., Ketchum K.A., In 1 2., In 1 2., In X., In X., Nelson D.L., Reese M.G., Reese M.G., Smith T., Smith T., Smith T., Shen H., Shen
Pancrusta Diptera; sophila.	STRAIN-Cregon-R; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases. Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases. [2] SEQUENCE FROM N.A. STRAIN-BERKeley; MEDLINE-20196066; Pubmed-10731132; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gall George R.A., Lewis S.E., Richards S., Ashburner M., Hender Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen E.	Brandon R.C., Rogers YH.C., Blazej R.G., Champe M., Ffeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Hellt G., Nelson C.R., Miklos G.L.G. Abril J.F., Agbayani A., An HJ., Andrews-Pfannkoch C., Baidwin D. Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beson K.I., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Cherty J.M., Cawley S., Daller H., Cadleu E., Center A., Chandra I Cherry J.M., Cawley S., Dathler C., Davenport L.B., Davis P., Dodgon R., Douch B.C., Dunn Jourbln K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Glorel A., Gorrell J.H., Gu Z., Gunn P., Harris M., Harris M., Larris M., Harris M., Elsen Harris M., Harris M.	Hostin D., Houston K.A., Howland T.J., Welf MH., Ibegwam C., Talali M., Kallush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum Klamel B.E., Kollush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum Klamel B.E., Kollush C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L. Nelson D.R., Nelson K.A., Nixon K., Muzny D.M., Nelson D.E., Should M., Pitthan G.S., Pan S., Pollard J., Puif V., Reese M. Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shue B.C., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Syler E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
252 A update on update on update of	nBank/D	al R.G., Andrews Andrews Bayrah Brokst Cadieu Davenpo Mays A., Gaz C., Gaz C.,	Ke Z., Kravit Kravit T.J., Well T.J., Moll Musske Noll N., Sl N.,
PRT; 252 AA. ed) snotherion update) annotation update) 3.4.21.4). 754. ult fly). udit fly). a, Endopterygota; a, Endopterygota; resophilidae; Dros	.; EMBL/Ge 731132; Holt R.P Holt R.P S., Li E Shards S	3.G. Blaze BJ., Jale J., Male J., Ferr Ilke C., Berr Garg N., D., D.,	" G H. T.
DROWE TRYI_DROME STANDARD; PRT; 252 AA. PP22905; Q9V5Y6; 01-OCT-1996 (Rel. 34, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) 10TA-TRY OR TRY-IOTA OR CG7754. Drossophila melanogaster (Fruit fly). Drossophila melanogaster (Fruit fly). ENEARYOR: Mercomorpha; Ephydroidea; Drospera; Endopterygota; Muscomorpha; Ephydroidea; Drosphilidae; Drosphilae; Drosphil	STRAIN-Oregon-R; Gao L., Wang S., Hickey D.A.; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ dat [2] SEGUENCE FROM N.A. STRAIN-BERKeley; STRAIN-BERKeley; AGAMS M.D., Celniker S.E., Holt R.A., Evans C.A., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Amenatides P.G., Scherer S.E., Li P.W., Hoskins R George R.A., Lewis S.E., Richards S., Ashburner M Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q.	ers YH.C. an, Baxter law, Baxen a P.V. Besen an M.R. Besen an D.A. Bute an D.A. Dute cher A. Donne Cher A. Donne cler	Hostin N., Rouston K.A., Howland T.J., Meinulez J. N., Hostin M., Ralush F., Karpen G.H., Re Z., Kennison Kinmel B.E., Kodra C.D., Kraft C., Kravitz S., Kland Lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Lidan Lasko P., Lel Y., Levitsky A.A., Li J., Li Z., Lidan Lau X., Mattei B., McIntosh T.C., McLeod M.P., McPh Merkulov G., Milshina N.V., Mobarry C., Morris J., Monnt S.M., Moy M., Murphy B., Murphy L., Muzny D.M. Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., I Pedarazolo M., Pittman G.S., Pan S., Polladd J., Pur' Rednert K., Remington K., Saunders R.D.C., Scheeler Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P Syler E., Spradling A.C., Stapleton M., Strong R., Syler B., Spradling A.C., Stapleton M., Strong R., Wang ZY., Wassarman D.A., Weinstock G.M., Weissenk Williams S.M., Woodage T., Worley K.C., Wu D., Yang
O9V5Y6; 09V5Y6; 996 (Rel.) 9096 (Rel.) 0002 (Rel.) 10ta precu OR TRY-IO 1.1 a melanog a; Metazoa Pterygota Pterygota Pterygota Pterygota 10-727;	gon-R; ng S., 1 (NOV-199 (NOV-199 RELEY; 196006; , Cellul) , Cellul)	C., Roge Doyle C., Agbaye , Agbaye , Basu , Bench , Botch , Cavl. E., Cavl. D. Del Del, Del, Doup L., Evan Gabrie Gabrie	Houston Kalush Holston Holston M. Mils M. Pitt Remin Siden Syradi M. Wassa M. Wassa
RESULT 1 TRYI_DROME AC P52905; O9V5X6; DT 01-OCT-1996 (Re- DT 01-OCT-1996 (Re- DT 15-JUN-2002 (Re- DE TYPS1N 10ta pro- GN IOTA-TRY OR TRY OS Drosophila mela OC Eukaryota; Meta- OC Eukaryota; Meta- OC Eukaryota; Meta- OC Muscomorpha; Ep. OX NCBI_TAXID=7227 RN [1] RP SEQUENCE FROM N	STRAIN-Oregon-R; Gao L., Wang S., Submitted (NOV-19; [2] SEQUENCE FROM N.A STRAIN-Berkeley; MEDLINE-20196006; Adams M.D., Celnil, Amanatides P.G., George R.A., Lewil, Sutton G.G., Worth	Wannen R. Abril J.F. Abril J.F. Ballew R.M Ballew R.M Borkova D. Cherry J.M Cherry J.M Cherry J.M Dodson K., Durbin K.J Fosler C., Ratch R., Regoldek A.,	Hantis N. H., Houston K. A. Jalail M., Kalush F., Kalmael B. E., Kodira C. Lasko P., Lei Y., Levitland B. E., Kodira C. Lasko P., Lei Y., Levitlin Merkulov G., Milshima N. Mount S. M., Moy M., Mun Nelson D. R., Nelson K. Palazzolo M., Pittman Grhert K., Remington Shue B.C., Siden-Kiamos Spier E., Spradling A. Gyurskas R., Tector C., Wang ZY., Wassarman I Williams S.M., Woodage
RESULT TRYILD TARYILD TO THE TARYILD TARXILD T	RA R	2	**************************************

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                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIK3_HUMAN STANDARD; PRT; 261 AA.
P07288; Q16272;
01-APR-1988 (Rel. 07, Created)
01-APR-1989 (Rel. 11, Last sequence update)
15-JUM-1989 (Rel. 41, Last annotation update)
Prostate specific antigen precursor (BC 3.4.21.77) (PSA) (Gamma-seminoprotein) (Kallikrein 3) (Semenogelase) (Seminin) (P-30 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Digry M.R., Zhang, X.Y., Ricchard R.,;
"Human prostate specific antigen (PSA) gene: structure and linkage to
the kallikrein-like gene, hGK-1.";
Nucleic Acids Res. 17:2137-2137(1989).
                                      SUBDINIT: MONOMER.
SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE DISTAL QUARTER
OF THE INTESTINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVATION PEPTIDE (POTENTIAL).
CHYMOTRYPSIN-LIKE SERINE PROTEINSE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           ENZYME REGULATION: ACTIVATED BY AN AUTOCATALYTIC MECHANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIRONES; SULLALL,
MIRONES; SULLALL,
InterPro; IPR001234; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
Fram; PR00089; trypsin; 1.
SMART; SM00202; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_INS; 1.
PROSITE; PS00134; TRYPSIN_INS; 1.
PROSITE; PS00135; TRYPSIN_INS; 1.
Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADAA9A8A22BEFCEC CRC64;
                                                                                                                                           SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1
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MEDLINE-89183632; PubMed-2467258;
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27250 MW;
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80.0%;
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PIR, S32750; S32750.
HSSP; P00763; 1DPO.
MEROPS; S01.121;
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254 AA;
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SEQUENCE
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                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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           Zheng L.,
Smith H.O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                           Groppe J.C., Morse D.E.;
"Molluscan chymotrypsin-like protease: structure, localization, and
substrate specificity.";
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SIMILARITY).
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chymotrypsin-like serine proteinase precursor (EC 3.4.21.-).
Hallotis rufescens (California_red abalone).
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Hallotidae; Hallotis.
NCBI_TaxID=6454;
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 1;
Pred. No. 0.14;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR001314; Chymotrypsin.
Interpro; IPR0001254; Ser_protease_Try.
Pfam: PF00089; trypsin; 1
PRINTS; PR00722; CHYMOTRYPSIN.
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MEDLINE-93343624; Pubmed-8342947;
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80.0%;
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EMBL; AE003826; AAF58655.1;
HSSP; P00763; 1DPO.
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P35003;
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  SECURNCE OF 1-176 FROM N.A.
MEDLINE-95079406; PubMed-7527295;
Monne M., Croce C.M., Yu H., Diamandis E.P.;
"Molecular characterization of prostate-specific antigen messenger RNA
                                                                                                                                                                                                                                                                                                                           TISSUE-Prostate;
MEDLINE-89165891; PubMed-2466464;
Riegman P.H.J., Vlletstra R.J., van der Korput J.A.G.M., Romijn J.C.,
                                                                                                          "Characterization of the gene for prostate-specific antigen, a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence of a cDNA clone encompassing the complete mature human prostate specific antigen (PSA) and an unspliced leader sequence."; Nucleic Acids Res. 16:6226-6226(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Monne M.M., Moreno J.M., Mele C.M., Mulholland G.M., Gomella L.G., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                     TISSUE-Prostate;
PUNDELINE-PE24651; PubMed-2470373;
Henttu P., Vikko P.;
"CDNA coding for the entire human prostate specific antigen shows high homologies to the human tissue kallikrein genes.";
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MEDLINE-20510030; PubMed-11054574;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
Gene 257:119-130(2000)
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SEQUENCE FROM N.A.
MEDLINE-89282407; PubMed-2471958;
Klobeck H.-G., Combriato G., Schulz P., Arbusow V., Fittler F.;
"Genomic sequence of human prostate specific antigen (PSA).";
Nucleic Acids Res. 17:3981-3981(1989).
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MEDLINE-88289366; PubMed-2456523;
Schulz P., Stucka R., Feldmann H., Combriato G., Klobeck H.-G.,
                                                                                                                                                                     MEDIINE-87190978; PubMed-2436946;
Lundwall A., Lilja H.;
"Molecular cloning of human prostate specific antigen cDNA.";
FEBS Lett. 214:317-322(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                             lochem. Biophys. Res. Commun. 161:1151-1159(1989)
                                                                          TISSUE-Leukocyte;
MEDLINE-89302090; PubMed-2472789;
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SEQUENCE OF 25-261.
MEDLINE-86205857; PubMed-2422647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer Res. 54:6344-6347(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed in breast tumors
                                                                                                                     glandular kallikrein."
                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                Lundwall A.;
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-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  3D-STRUCTURE MODELING.
MEDLINE-95218633; PubMed-7535613;
Villoutrelx B.O., Getzoff B.D., Griffin J.H.;
"A structural model for the prostate disease marker, human prostate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD-STRUCTURE MODELING.
MEDLINE=98427950; PubMed=9751643;
COOMDS G.S., Bergstrom R.C., Pellequer J.L., Baker S.I., Navre M.,
Smith M.M., Tainer J.A., Madison E.L., Corey D.R.;
"Substrate specificity of prostate-specific antigen (PSA).";
Chem. Biol. 5:475-488(1998).
-i- FUNCTION: PRESUMABLY HYDROLYZE THE HIGH MOLECULAR MASS SEMINAL
VESICLE PROTEIN THUS LEADING TO THE LIQUEFACTION OF THE SEMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prints, PR0089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SNART; SM00720; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOW; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Glycoprotein; Antigen; Zymogen; Signal;
                                                                                                                                                                                                                  MEDLINE-88082806; PubMed-3691515; Schaller J., Akiyama K., Tsuda R., Hara M., Marti T., Rickli E.E.; Schaller J., Akiyama K., Tsuda R., Hara M., Marti T., Rickli E.E.; Isolation, characterization and amino-acid sequence of gamma-seminoprotein, a glycoprotein from human seminal plasma."; Eur. J. Biochem. 170:111-120(1987).
Watt K.W.K., Lee P.J., M'Timkulu T., Chan W.P., Loor R.; "Human prostate-specific antigen: structural and functional similarity with serine proteases."; Proc. Natl. Acad. Sci. U.S.A. 83:3166-3170(1986).
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InterPro; IPR001254; Ser_protease_Try.
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X13941; CAA32124.1; ALT_SEQ.
X13942; CAB46487.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specific antigen.";
Protein Sci. 3:2033-2044(1994).
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BC005307; AAH05307.1;
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X05332; CAA28947.1;
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PIR; A32423; A32423.
PDB; 1PFA; 26-JAN-95.
PDB; 2PSA; 16-MAR-99.
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A26757; A26757
                                                                                                                                                                                            SEQUENCE OF 25-261.
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261 AA;
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SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE-93363642; PubMed=7689340;
Gauthler E.R., Chapdelaine P., Tremblay R.R., Dube J.Y.;
Eduthler E.R., Chapdelaine P., Tremblay R.R., Dube J.Y.;
Biochim. Blophys. Acta 1174:207-210(1993).
I-FUNCTION: PSA PRESUMABLY HYDROLYEE THE HICH MOLECULAR MASS
SEMINAL CASICLE PROTEIN THUS LEADING TO THE LIQUEFACTION OF
THE SEMINAL COAGULUM. PSA IS A GLANDULAR RALLIRREIN.
I-CATALYTIC ACTIVITY: PREferential cleavage: Tyr-1-Kaa.
I-SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. KALLIRREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                    PROSTATE SPECIFIC ANTIGEN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Frostate specific antigen precursor (EC 3.4.21.35) (PSA) (Gamma-seminoprotein) (Kallikrein 3).
KLK3 OR APS.
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-> D (IN REF. 5).
AE9E732AF872141A CRC64;
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80.0%;
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PIR; S34239; S34239.
PIR; S35711; S35711.
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Matches 8; Conservative
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261 AA;
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209 CSGDSGGPLV 218
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Gaps
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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MEDLINE-94289349; PubMed-8018603;
MEDLINE-94289349; PubMed-8018603;
Sato T., Matsushita M., Fujita T.;
"Molecular characterization of a novel serine protease involved in activation of the complement system by mannose-binding protein.";
Int. Immunol. 6:665-669(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRAR_HUMAN STANDARD; PRT; 699 AA.
P48740; 095570; G9PTE09;
01-FEB-1996 (Rel. 33, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-OCT-2011 (Rel. 40, Last sequence update)
16-OCT-2011 (Rel. 40, Last sequence update)
16-OCT-2011 (Rel. 40, Last sequence update)
16-OCT-2011 (Rel. 40, Last section protesse protesse plot) (RaRF)
16-OCT-2011 (Mannose-binding protein maspl OR CRARF OR CRARFIOR PRSS5.
                                                                                                                                                                                                                                               Hydrolase; Serine protease; Glycoprotein; Antigen; Zymogen; Signal
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MEDLINE-94059062; PubMed-8240317;
Takada F., Takayama Y., Hatsuse H., Kawakami M.;
An new member of the Cls family of complement proteins found in a bactericidal factor, Ra-reactive factor, in human serum.";
Biochem. Biophys. Res. Commun. 196:1003-1009(1993).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL). 8525B14B15967E5C CRC64;
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"Exon structure of the gene encoding the human mannose-binding
protein-associated serine protease light chain: comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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0; Mismatches
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PR00089; trypain; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPC; 1.
PROSITE; PS02040; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
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MEDLINE-97079701; PubMed-8921412;
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Int. Immunol. 8:1355-1358(1996)
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Best Local Similarity 80.uv,
8; Conservative
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. pathway; Serine protease; Protease;
Repeat; Signal; EGF-like domain; Hydroxylation.
9
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70 KDA CHAIN OF P100 (P70).

29 KDA CHAIN OF P100 (P29).

20TB 1.

EGF-LIKE, CALCIUM-BINDING (POTENTIAL).

CUB 2.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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80.0%; Pred. No. 0.37;
1.ve 0; Mismatches 2; Indels
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(IN REF. 3)
(IN REF. 2)
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 InterPro; IPR001254; Ser_protease_Try
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                   SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00110; ASX_HYDROXYL; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01187; EGF_2; 1.
PROSITE; PS01187; EGF_2; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
Hydrolase; Complement pathway; Serink Glycoprotein; Sushi; Repeat; Signal;
                           Pfam; PP00084; susht; 2.
Pfam; PP00089; trypsin; 1.
Pfam; PP00431; CUB; 2.
PRINTS; PR00722; CHYMOTRPSIN.
SMART; SM00032; CCP; 2.
SMART; SM00041; CUB; 2.
SMART; SM00181; EGF; 1.
SMART; SM00181; EGF; 1.
SMART; SM00179; EGF
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Best Local Similarity 80.0
Matches 8; Conservative
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699 AA;
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CRAR_MOUSE
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                                        Takayama Y., Takada F., Nowatari M., Kawakami M., Matsu-ura N.;

Takayama Y., Takada F., Nowatari M., Kawakami M., Matsu-ura N.;

"Gene structure of the P100 serine-protease component of the human Raractive factor."

"Emanuol. 36:505-514(1999).

-I- FUNCTION: COMPONENT OF THE BACTERICIDAL RA-REACTIVE FACTOR RARF

WHICH SPECIFICALLY BINDS TO RA AND R2 POLYSACCHARIDES EXPRESSED BY

CERTAIN ENTERORACTERIA. IT TRIGGERS THE ACTIVATION OF COMPERMENT

CASCADE BY ACTIVATING THE C4 AND C2 COMPONENTS. IT ACTIVATES THE

C4 COMPONENT BY CIRCLY THE ALEPHA-CHAIN OF C4.

C1 COMPONENT BY CIRCLY STATES OF A COMPLEMENT-ACTIVATING COMPONENT.

C1 CHARF) AND A POLYSACCHARIDE-BINDING (MANNOSE-BINDING) COMPONENT.

C1 COMPAIN: CRARF HAS A MODULE ORGANIZATION SIMILAR TO CIR AND C1S.

ILINED BY A DISULFIDE BOND.

C1 DOWAIN: CRARF HAS A MODULE ORGANIZATION SIMILAR TO CIR AND C1S.

C1 SIMILARITY: CONTAINS 2 USB DOMAINS.

C1 SIMILARITY: CONTAINS 2 USB DOMAINS.

C1 SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB010822; BAA34864.1; JOINED.
AB010813; BAA34864.1; JOINED.
AB010815; BAA34864.1; JOINED.
AB010815; BAA34864.1; JOINED.
AB010816; BAA34864.1; JOINED.
AB010817; BAA34864.1; JOINED.
AB010819; BAA34864.1; JOINED.
AB010819; BAA34864.1; JOINED.
AB010820; BAA34864.1; JOINED.
AB010821; BAA34864.1; JOINED.
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[4]
SEQUENCE FROM N.A.
MEDLINE-99402590; Pubmed-10475605;
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InterPro: IPR001859; CUB_domain.
InterPro: IPR001314; Chymotrypsin.
InterPro: IPR000561; EGF-like.
InterPro: IPR001881; EGF_Ca.
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MEROPS; S01.
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EMBL;
EMBL;
EMBL;
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EMBL;
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Gaps

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(POTENTIAL) (POTENTIAL) (POTENTIAL Q

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SMART; SW00020; Tryp_SPC; 1.
PROSITE; PS00100; ASX_HYDROXYL; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01187; EGF_C3; 1.
PROSITE; PS01187; EGF_C3; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_BIS; 1.
PROSITE; PS00135; TRYPSIN_SIS; 1.
Hydrolase; Complement pathway; Serine protease; Protease; Glycoprotein; Sushi; Repeat; Signal; EGF-like domain; Hydroxylation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Limulus clotting factor C precursor (EC 3.4.21.84) (FC).
Carcinoscorplus rotundicanda (Southeast Asian horseshee crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
                                                                                                                                                                                                                                                                        70 KDA CHAIN OF P100 (P70).
29 KDA CHAIN OF P100 (P29).
CUB 1.
EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA from the
                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         · · · ) (POTENTIAL)
                                                                                                                                                                                                                                    COMPLEMENT-ACTIVATING COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 1; Length 704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ding J.L., Navas M.A. III, HO B.;
"Molecular clounds and sequence analysis of factor C cDNA
"Singapore horseshoe crab, Carcinoscorpius rotundicauda.";
Mol. Mar. Biol. Blotechnol. 4:90-103(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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N-LINKED (GLCNAC.
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SUSHI 1.
SUSHI 2.
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MEDLINE-95268506; PubMed-7538401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79895 MW;
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80.0%;
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704 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6848;
                                                                                                                                                                                            Glycoprotein;
SIGNAL
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026422;
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CARBOHYD
SEQUENCE
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CARBOHYD
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Matches
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-1- FUNCTION: COMPONENT OF THE BACTERICIDAL RA-REACTIVE FACTOR RARF WHICH SPECIFFCALLY BINDS TO RA AND R2 POLYSACCHARIDES EXPRESSED BY CERTAIN ENTERCOBACTERIA. IT TRIGGERS THE ACTIVATION OF COMPLEMENT CASCADE BY ACTIVATING THE C4 COMPONENTS. IT ACTIVATES THE C4 COMPONENT BY CLEATIVATING THE ALPRA-CHIN OF C4.

-1- SUBJUNT: RARF CONSISTS OF A COMPLEMENT-ACTIVATING COMPONENT. CASUBLY SACHED BOND.

-1- SUBJUNT: RARF CONSISTS OF A COMPLEMENT-ACTIVATING COMPONENT. CRARF IS AN HETERODIMER OF A HEAVY (P70) AND A LIGH CHAIN (29)

-1- SUBJUNT: LIVER.

-1- DOMAIN: CRARF HAS A MODULE ORGANIZATION SIMILAR TO CIR AND CIS.

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

-1- SIMILARITY: CONTAINS 2 USB DOMAINS.

-1- SIMILARITY: CONTAINS 2 USB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement'is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAINF-BALB/C, TISSUE-LIVER;
MEDLINE-94179811; PubMed-8133044;
Takayama Y., Takada F., Takahashi A., Kawakami M.;
Takayama Y., Takahashi A., Takahashi A., Kawakami M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-93176166; Pubmed-8439319;
Takahashi A., Takayama Y., Hatsuse H., Kawakami M.;
"Presence of a serine protease in the complement-activating component of the complement-dependent bactericidal factor, RaRF, in mouse
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Complement-activating component of Ra-reactive factor precurso (EC 3.4.21.-) (Ra-reactive factor serine protease pl00) (RaRF)
(Mannan-binding lectin serine protease 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 465-704 FROM N.A., AND PARTIAL SEQUENCE
        704 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; IPR001254; Ser_protease_Try.; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; r.,
MEROPS; S01.198; -.,
MGD; MG1188492; Maspl.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001314; Chymotrypsin. IPR000561; EGF-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunol. 152:2308-2316(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D16492; BAA03944.1; -. HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00084; sushi; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF00431; CUB; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF_CA; 1
      STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00032; CCP; 2.
                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
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Gaps

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FUNCTION: THIS ENZYME IS CLOSELY ASSOCIATED WITH AN ENDOTOXINSENSITIVE HEMOLYMPH COAGULATION SYSTEM WHICH MAY PLAY IMPORTANT ROLES IN BOTH HEMOSTASIS AND HOST DEFENSE MECHANISMS. ITS ACTIVE FORM CATALIZES THE ACTIVATION OF FACTOR B. CATALIZES THE ACTIVATION OF FACTOR B. CATALIZES FORM THE ACTIVATION OF FACTOR B. CATALIZES Selective cleavage of 103-Arg-|-Ser-104 and 124-Ile-|-Ile-125 bonds in Limulus clotting factor B to form activated factor B. Cleavage of Pro-Arg-|-Xaa bonds in synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEAVY CHAIN LIGHT CHAIN
                                                                                                            substrates.
--- ENEXME REGULATION: ACTIVATED BY GRAM-NEGATIVE BACTERIAL LIPOPOLYSACCHARIDES AND CHYMOTRYPSIN (BY SIMILARITY).
--- SUBBUNIT: HETERODIMEN OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISTLETDE BOND (BY SIMILARITY).
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
--- SIMILARITY: CONTAINS 5 SUSHI (SCR) DOMAINS.
--- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
--- SIMILARITY: CONTAINS 1 LGCL DOMAIN.
--- SIMILARITY: CONTAINS 1 LGCL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
SUBSTRATE (BY SIMILARITY).
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A CHAIN.
B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Serine protease; Signal; Lectin; Hemolymph clotting; Glycoprotein; Cell adhesion; EGF-like domain; Sushi; Repeat.
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LIMULUS CLOTTING FACTOR C,
LIMULUS CLOTTING FACTOR C,
LIMULUS CLOTTING FACTOR C,
LIMULUS CLOTTING FACTOR C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; SUI.415;
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001043; EGF-like.
InterPro; IPR001304; Lectin_C.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF000084; Sushi, Sc.
Pfam; PF000089; Lrypsin; 1.
Pfam; PF000089; Lrypsin; 1.
Pfam; PF000099; Lrypsin; 1.
PRNO717; SM000131; CGP, 5.
SMART; SM001031; CGP, 5.
SMART; SM001031; CGP, 5.
SMART; SM001031; CGP, 5.
PROSITE; PS000120; Tryp_SPC; 1.
SMART; SM001020; Tryp_SPC; 1.
PROSITE; PS000120; Tryp_SPC; 1.
PROSITE; PS000120; CGF_1; 1.
PROSITE; PS00134; TRYPSIN_IS; 1.
PROSITE; PS00134; TRYPSIN_IS; 1.
PROSITE; PS00134; TRYPSIN_IS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-TYPE LECTIN.
SUSHI 4.
SUSHI 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
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SUSHI 2.
SUSHI 3.
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MEDLINE-91177916; PubMed-2007602;
MEDLINE-91177916; PubMed-2007602;
MAIDATA T., MISUAH T., MISUAH T., Tokunaga F., Nakamura T., Toh Y.,
MISUAH T., MISUAH T., MISUAH T., Tokunaga F., Nakamura T., Toh Y.,
Ikehara Y., Iwanaga S.;
"Limulus factor C. An endotoxin-sensitive serine protease zymogen
With a mosals structure of complement-like, epidermal growth
factor-like, and lectin-like domains.";
J. Biol. Chem. 266:6554-6561(1991).
J. Biol. Chem. 266:6554-6561(1991).
J. Biol. Chem. 266:6554-6561(1991).
J. Biol. Chem. 266:6554-6561(1991).
C. FURM CATALYZES THE RACIVARIE NOST DEFENSE MECHANISMS. ITS ACTIVE
FORM CATALYZES THE ACTIVATION OF FACTOR B.
C. CATALYTIC ACTIVITY. Selective cleavage of 103-Arg-|-Ser-104 and
MACHALYZES THE ACTIVATION OF CLEAVAR DESCRIPTION OF ACTIVE
FORM CATALYZES THE ACTIVATION OF FACTOR B.
C. CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-|-Ser-104 and
MACHALYZES THE ALLA-|-III-125 bonds in Limnlus clotting factor B to form
Activated factor B. Cleavage of Pro-Arg-|-Xaa bonds in synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last sequence update)
Limulus clotting factor C precursor (EC 3.4,121.84) (FC).
Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota: Metazoa; Arthropoda; Chellcerata; Merostomata; Xiphosura;
NCBL_TaxID-6853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            substrates.
-!- ENZYME REGULATION: ACTIVATED BY GRAM-NEGATIVE BACTERIAL LIPOPOLISACCHARIDES AND CHYMOTRYPSIN.
-!- SUBDNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND.
                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   918A1ED8B817B6C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-i- SIMILARITY: CONTAINS 5 SUSHI (SCR) DOMAINS.
-i- SIMILARITY: CONTAINS I C-TYPE LECTIN FAMILY DOMAIN.
-i- SIMILARITY: CONTAINS I EGF-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS I LCCL DOMAIN.
BY SIMILARITY.
BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB :
Pred. No. 0.54;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1019 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                      112429
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 94.0
Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFC_TACTR P28175;
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CARBOHYD
SEQUENCE
                                                                                     DISULFID
                                                                                                                                      DISULFID
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        DISULFID
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962 CSGDSGGPLV 971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-9615;
                                   1 CXGDSGGPXV
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Q28278;
                                                                                                                                                                                                                                                        EL2B_HORSE
P37358;
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SEQUENCE
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LIGHT CHAIN.
A CHAIN.
B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
SUBSTRATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
LITTWIG -> TDNVTAI (IN SHORI ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; FALSE_NEG.
PROSITE; PS001186; EGF_2; FALSE_NEG.
PROSITE; PS0020; LCCL; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_BIS; 1.
Hydrolase; Serine protease; Signal; Alternative splicing; Lectin; Sush; Repeat.
Sush; Repeat.
1 25
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Pred. No. 0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIMULUS CLOTTING FACTOR C.
LIMULUS CLOTTING FACTOR C, ILIMULUS CLOTTING FACTOR C, LIMULUS CLOTTING FACTOR C, B.
LIMULUS CLOTTING FACTOR C, B.
EMF-LIKE.
SUSHI 1.
SUSHI 1.
SUSHI 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1019 AA; 112346 MW; 5BC2864C6715289B CRC64;
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BY
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C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-TYPE LECTIN.
SUSHI 4.
SUSHI 5.
                                                                                                                                                                                                                                     InterPro; IRR004043; LCCL_dom.
InterPro; IPR001304; Lectin_C.
InterPro; IPR001304; Ser_protease_Try.
InterPro; IRR000124; Ser_protease_Try.
Pfam; PF00005; lectin_C; l.
Pfam; PF00089; Ltypsin; 5.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00032; CCP; 5.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                   InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-like.
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80.0%;
EMBL; D90271; BAA14315.1;
EMBL; D90272; BAA14316.1;
                                                                                                                            HSSP; P00763; 1DPO
                                                                                                                                                             MEROPS; S01.219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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Gaps

; 0

2; Indels

0; Mismatches

Similarity 80.0 8; Conservative

Best Local Matches

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SEQUENCE FROM N.A.
MEDLINE=94318474; PubMed=8043441;
Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
A comparative study of partial primary structures of the catalytic region of mammalian protein C.,
Br. J. Haematol. 86:590-600(1994).
-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                            TISSUE-Neutrophils;
MEDLINE-94271153; PubMed-7516152;
Dubin A., Potempa J., Travis J.;
"Structural and functional characterization of elastases from horse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNC-1095 (Rel. 41, Last annotation update)
15-UNC 2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                         neutrophis.";
Biochem. J. 300:401-406(1994).
1- FUNCTION: MAY BE INVOIVED IN THE DEGRADATION OF CONNECTIVE
TISSUE IN CHRONIC LONG DISEASE.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.
                                      01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Neutrophil elastase 2B (EC 3.4.21.-) (Proteinase 2B) (Fragments).
Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 1; Length 73; Pred. No. 0.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARGE RELAY SYSTEM.
AFFB0B330DB69041 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 AA.
73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S44462.
HSSP; P00766; 1GCD.
MEROPS; S01.131;
Interpro; IPR001254; Ser_protease_Try.
PROSITE; PS50240; TRYPSIN_DOM; PARTIAL.
PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 AA; 7615 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase, Serine protease NON_CONS 31 32 NON_CONS 56 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 92.0
Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994).
-!- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIFIEDS.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VILIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94318474; PubMed-8043441;
Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
41, Last annotation (Rel. 34, 21.69)
41, Last annotation (Rel. 34, 21.69)
                                    -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                           PREMI; PRO0089; Trypsin; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS0014; TRYPSIN_DOW; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 1; Length 157;
Pred. No. 0.13;
0; Mismatches 2; Indels
                                                                    -i- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17262 MW; E8B1BACF49220DFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARGE RELAY SYSTEM
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 AA
                                                                                                                                                                                                                                                                                            MEROPS; S01.218; -. InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                            EMBL; D43751; BAA07808.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.0%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 1
157 AA;
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                                                      and VIIIa
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Q28315;
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ACT_SITE
DISULFID
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TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

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                               between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murakawa M., Okamura T., Kamura T., Kurolwa M., Harada M., Niho Y.,
"A comparative study of partial primary structures of the catalytic
region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994).
-!- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
-!- CATALITIC ACTIVITY: Degradation of blood coagulation factors Va
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
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BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                     Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
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-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17251 MW; B89790F9954B610A CRC64;
                                                                                                                                                                                                                                                                                                                                                                          CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 1;
Pred. No. 0.13;
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                                                                                                                                                                                                                      InterPro; IPR001254; Ser_protease_fry.
Pfam; PF00089; trypsin; 1.
SMARY; SM0020; Tryp_SPC; 1.
PROSITE; PS00120; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1.
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Best Local Similarity 80...
Best Local 8, Conservative
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ACT_SITE
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SEQUENCE
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Blood coagulati
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Q28506;
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ACT_SITE
DISULFID
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PRTC_MACMU
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Br. J. Hacmatol. 86:590-600(1994).
-!- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGLATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
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Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Vitamin K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                     CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW; FBDC5BE2ECA74BB4 CRC64;
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Pred. No. 0.13
0; Mismatches
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                                                                                                                        InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
SWART; SW00020; Tryp_SPS; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER: 1.
  email to license@isb-sib.ch).
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Pfam; PF00089; trypsin; 1.
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80.0%;
                                                  EMBL; D43750; BAA07807.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CEGDSGGPMV 130
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Best Local Similarity
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                                                                                                        MEROPS; S01.218
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028380;
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SEQUENCE
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DWN-2002 (Rel. 41, Last annotation update)
42, Last annotation IIA)
43, Last annotation (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94318474; PubMed-8043441;
Murakawa M., Okamura T., Ramura T., Rurolwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1.
Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
NON_TER
                                                                        Hydrolase
                                                                                                                                                                                                                                                                     Score 46; DB 1; Length 157;
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                                                                                                                                                                                                                                                                                                       . 2; Indels
                                                                                                                                                                                                                                  BFAA6EA045C3C580 CRC64;
                                                                     Glycoprotein; Serine protease;
                                                                                                      CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                      Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 AA
                                                                                                                                                                                                                                                                                                       0; Mismatches
SMART; SM00020; TIYP_SPC; 1.
PROSITE; PSSO40; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1.
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Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                  17200 MW;
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80.0%;
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                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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157 AA;
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96
121
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(See http://www.lsb-sib.ch/announce,
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European Bioinformatics Institute. There are no restrictions on
by non-profit institutions as long as its content is in no
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CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
REQUIRED FOR SPECIFICITY (BY SIMILARITY).
26160BlaFF80FICD CRC64;
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                   Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Musconorpha; Oestroidea; Calliphoridae; Lucilia
                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.

BY SIMILARITY.

N-LIKKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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larity 80.0%; Pred. No. 0.13;
Conservative 0; Mismatches 2; Indels
                                                                                                                 Score 46; DB 1; Length 161;
Pred. No. 0.13;
0; Mismatches 2; Indels
                                                                                         27D78F185B2FCC69 CRC64;
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1
                                                                                                                                                                                                                                                                                                  )1-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
hrypsin alpha-3 (EC 3.4.21.4) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease; Multigene family.
                                                                                                                                                                                                                                                             165 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long amodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (sor send an email to license(lsb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WART; SM00020; TIYP_SPC; 1.
PROSITE: PSSO40; TRYPSIN_DOM; 1.
PROSITE: PS00134; TRYPSIN_SER; 1.
PROSITE: PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro; IPR001254; Ser_protease_Try
                                                                                                                                                                                                                                                              PRT;
26 CH
129 CH
114 BY
153 BY
17 N-
82 N-
161 1770 MW;
                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                 92.0%;
80.0%;
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                                                                                                                                            Conservative
                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fam; PF00089; trypsin;
                                                                                                      Query Match
Best Local Similarity
----s 8; Conserv?
                                                                                                                                                                                   125 CEGDSGGPMV 134
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 AA;
                                                 17
82
161
161 AA;
                                                                                                                                                                    1 CXGDSGGPXV 10
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EROPS; S01.112;
                                                                                                                                                                                                                                                                                                                                                                                         MCBI_TaxID-7375;
                                                                                                                                                                                                                                                                                    01-FEB-1994
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                                                 CARBOHYD
CARBOHYD
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SEQUENCE
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DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
                                                                                                                                                                                                                                                                         935043;
                                                                                                                                                                                                                                   RESULT 15
TRY3_LUCCU
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Gaps

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1 CXGDSGGPXV 10

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| |||||| | 115 CQGDSGGPLV 124 셤 Search completed: May 12, 2003, 15:36:38 Job time : 6.8 secs

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Gencore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2003, 15:32:37 ; Search time 22.6 Seconds

(without alignments)
91.171 Million cell updates/sec

Title: US-09-909-348-2
Sequence: 1 CxGDSGGPXV 10
Scoring table: BLOSUM62
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580
Minimum DB seq length: 0
Maximum DB seq length: 0
Maximum DB seq length: 0
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries
```

3: sp_fung1:*
4: sp_human.*
5: sp_human.*
6: sp_nammal.*
7: sp_nammal.*
8: sp_nammal.*
8: sp_nammal.*
10: sp_nammal.*
11: sp_rodent.*
12: sp_virus.*
13: sp_virus.*
14: sp_virus.*
15: sp_rotentap.*
16: sp_rotentap.*
17: sp_acteriap.*
17: sp_acteriap.*
18: sp_acteriap.*
19: sp_acteriap.*
17: sp_acteriap.*

SPTREMBL_21:* 1: sp_archea:* 2: sp_bacteria:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	097399 phaedon coc	098dll rhizobium l	Ogvaco drosophila	018458 heterodera	016126 boltenia vi			_	_	-			_	_	_		
	-	• • • • • • • • •																
	£ £	097399	Q98DL1	09VGC0	018458	016126	09VQ98	Q95UP4	Q9VRS8	Q9VRD0	Q9VRD1	Q9VRS9	016101	Q9VMX7	017030	Q9V4W5	088264	
	æ		16	Ŋ	ខ	ഗ	ស	S.	'n	Ŋ	S	S	S	S	'n	Ŋ	ນ	
	luery Match Length DB	258	152	214	247	248	248	254	259	259	260	262	265	266	268	271	272	
æ	Query Match	96.0	94.0	94.0	94.0	94.0	94.0	94.0	94.0	94.0	94.0	94.0	94.0	94.0	94.0	94.0	94.0	
	Score	48.	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	
	Result No.	1	7	m	7	2	9	7		თ	. 10	11	12	13	14	12	16	

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0; Gaps

Query Match 96.0%; Score 48; DB 5; Length 258; Best Local Similarity 80.0%; Pred. No. 0.29; Matches 8; Conservative 0; Mismatches 2; Indels ·

097398 phaedon coc Q9vmx8 drosophila Q9vmx8 drosophila Q9vtv2 drosophila Q8t508 aedea aegyp Q82082 mus musculu 966088 haemaphysal Q9463 drosophila Q9vx14 drosophila Q9vx84 drosophila Q9vx84 drosophila Q9vx87 drosophila Q9vx87 drosophila	10 2000
6 5 097398 6 5 09VAX8 6 1 09DA13 7 5 09VTV2 6 1 09AT906 6 1 09AT906 5 5 09W453 2 5 09W453 2 5 09VX10 3 6 09VX10 3 5 09VX10	111 5 Q9VZSB 11 Q9VZSB 11 Q9JZ9 14 5 Q9VX10 17 5 Q9VX10 18 5 Q26423 19 5 Q9VZES 10 5 Q9VZES 10 6 Q9VZES 11 Q6GTK6 10 Q6GTK6 10 01 Q9TK9 11 13 Q9PUF3 11 13 Q9PUF3 12 Q9VRSB 13 Q9PUF3 14 Q9NRSB 18 Q9DVZSS 19 Q9VZSS 11 Q9DVZSS 11 Q9DVZSS 12 Q9DVZSS 13 Q9DVZSS 14 Q9NRSB
47 94.0 276 47 94.0 2872 47 94.0 2872 47 94.0 2874 47 94.0 2874 47 94.0 345 47 94.0 345 47 94.0 4125 47 94.0 4136 47 94.0 4136 47 94.0 4136 47 94.0 4136	47 94.0 611 47 94.0 701 47 94.0 701 47 94.0 704 47 94.0 10813 47 94.0 1190 46 92.0 50 46 92.0 66 46 92.0 73 46 92.0 66 46 92.0 1170 46 92.0 1170 46 92.0 1170
114 223 223 224 225 227 30 30	000000000044444 10000000044444 100000000

ALIGNMENTS

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TRYPSIN FAMILY
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018458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gutten R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D., Wan K.H., Doyle C., Baxter E.G., Hellt G., Nelson C.R., Mikhos G.L.G., Abril J.F., Agbayan A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beason K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
                                                                                                                                                                                                                                                                                                                       Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 16; Length 152;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 7:331-338(2000).
EMBL; AP003004; BAB51260.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 152 AA; 16393 MW; E74A9FF9E5567A1F CRC64;
                                                                                                                                                                                                                                 01-OCT-2001 (TTEMBLrel. 18, Last sequence update)
01-MAR-2002 (TTEMBLrel. 20, Last annotation update)
Hypothetical protein mlr4654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                        152 AA
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                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21082930; PubMed-11214968;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.0%;
80.0%;
                                                                                                                                                                                                             01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 80.
                                                                                                                                                                        PRELIMINARY;
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                                                       209 CSGDSGGPAV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesorhizobium lot1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Matches
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Gaps
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Sukryvota: Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
NCBI_TaxID-51029;
Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECTENCE FROM N.A.

MEDLINE-98030247; PubMed-9364965;
Lilley C.J., Orwin P.E., Atkinson H.J., McPherson M.J.;
Characterization of cDNAs encoding serine proteinases from the soybean cyst nematode Heterodera glycines.";
Mol. Blochem. Parasitol. 89:195-207(1997).

EMBL; Y13907; CAA74205.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 5; Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23006 MW; 06905997C4EA64C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS, PRO0722; CHYMOTREPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DON, 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ESF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003695; AAF54763.1; -. HSSP; P00766; 1CHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FBgn0038001; CG17404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TEMBLrel. 05, (01-JAN-1998 (TEMBLrel. 05, 101-JUN-2002 (TEMBLrel. 21, 18eria proteinase precursor. SP-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 80.0 ses 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 CSGDSGGPLV 169
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Diptera; Brachycera; Muscomorpha;

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Eukaryota, Metazoa, Arthropoda, Tracheata,
Pterygota, Neoptera, Endopterygota, Diptere
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 CSGDSGGPLV 203
                                                  NCBI_TaxID-7227;
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Q95UP4
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                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The Molecular Evolution of the Vertebrate Trypsinogens.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                              94.0%; Score 47; DB 5; Length 247; 80.0%; Pred. No. 0.43; 1.ve 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                    POTENTIAL.
SERINE PROTEINASE.
; 3A2B5B2B3BB77222 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Boltenia.
NCBL_TaxID=63515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 248 TRYPSIN 1.
248 AA; 25872 MW; AC606B8998413305 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VQ98 PRELIMINARY; PRT; 248 AA. Q9VQ98; 01-MAY-2000 (TrEMBLrel. 13, Created) 11-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) CG10882 protein.
                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
HSSP; P00763; 1DPO.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; tryps.n: 1.
SWART; SW00020; Tryp_SPC: 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF011897; AAB69653.1; -. HSSP, P00763; IDPO.
INTERPO. IPRO01314; Chymotrypsin.
InterPo: IPR001314; Chymotrypsin.
InterPo: IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRNTNS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp.SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
                                                                                                                                                   247 AA; 25586 MW;
                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                         Local Similarity 80.0 nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              Trypsinogen 1 precursor.
                                                                                                                                                                                                                                                                 201 CSGDSGGPLV 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 CQGDSGGPAV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                     1 CXGDSGGPXV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXGDSGGPXV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                         Boltenia villosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roach J.C.;
                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                     016126
016126;
                                                                                                                        SIGNAL
                                                                                                                                                                                                        Matches
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1D 099098
DT 011
DT 011
DE CG
                                                                                                                                                                                                                                                                                                                         016126
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Amanatides P.G., Scherer S. E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S. E., Il P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortuan J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
R.A. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Helt G., Nelson C.R., Miklos G.L.G.,
R.A. Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.W., Banos P.V., Berman B.P., Bhandari D., Bolshakov S.,
R. Ballew R.W., Callew B.P., Brottler P.,
R. Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
R. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
R. Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
R. Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A botson K.J. Evongelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
R.A. Goog F., Gorrell J.H., Gu Z., Guan P., Harris M.,
R.J., Harvey D., Helman T.J., Hernandez J.R., Houven C.,
A diali M., Kalush F., Karpen G.H., Ke Z., Rennison J.A., Retchum R.A.,
A lostin D., Houston R.A., Howland T.J., Wei M.-H., Ibeywam C.,
Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R. Mammel B.E., Kodira C.D., Kraft C., McLeod M.P., Mopherson D.,
Monte S. M., Maynh, P. M., Maynh, P. Moshert S. M.,
Monte S. M., Maynh, P. Maynh, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mount S.M., Moy M., Murphy B., Mirphy L., Mazhy D.M., Nelson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Spradiling A.C., Staplecon M., Skupski M.P., Smith T.,
Spradiling A.C., Staplecon M., Skupski M.P., Smith T.,
A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
X ed., Xeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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SEQUENCE 248 AA; 26744 MW; 07B0FD663F005807 CRC64;
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InterPro; IPR001254; Ser_protease_Try.
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PROSITE; PS00134; TRYPSIN HIS; UNR
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003583; AAF51279.1; -. HSSP; P00763; 1DPO.
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SEQUENCE FROM N.A.
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STRAIN-BERKELEY
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      SO OR REPAREMENT OF SO OR SO O
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yachards S.P., Ashburner M., Henderson S.N.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
Am K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
Ballew R.M., Basu A., Buck J., Brokstein P., Bolshakov S.,
Ballew R.M., Basu D.A., Buller B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Boolson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Allaris N.L., Harrisy D., Heiman T.J., Well M.-H., Ibbeywam C.,
Allaris N.L., Howlind T.J., Well M.-H., Ibbeywam C.,
Allali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
                                                                                                                                                                                                                             Stomoxys calcitrans (Stable fly).

Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Muscoidea; Muscidae; Stomoxys.

NCBL_TaxID=35570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Petrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     PROJUENCE FROM N.A.

Hamilton J.V., Munks R.J.L., Lehane S.M., Lehane M.J.;

*Association of Intestinal Defensin with a Novel Serine Protease in Submitted of UL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: AY044834; AAK98781.1;

Interpro; IPR001254; Ser_protease_Try.

Fram; PR00089; trypsin, 1.

PROSITE; PS50240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_LHIS; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.0%; Score 47; DB 5; Length 254;
80.0%; Pred. No. 0.45;
.ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Protease; Serine protease.
SEQUENCE 254 AA; 27521 MW; 99AAE8B1481FA439 CRC64;
                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
   254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 AA
   PRT;
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MEDLINE-20196006; Pubmed-10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
   PRELIMINARY;
                                                                                                                                                               Serine protease Ssp3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 CRGDSGGPAV 215
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXGDSGGPXV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG6580 protein.
                                                                                          01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Q95UP4
Q95UP4;
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liak X., Martel B. W. McIncoh T.C., Moreso D.,
RA Merkulov G., Milshina N.V., Moberry C., Morris J., Moshrefi A.,
RA Melson D.K., Nalson K.B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Parle D.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Stden Fflamos I., Simpson M., Stwigski M. P., Smith T.,
RA Spier E., Stradling A.C., Stapleton M., Strong R., Sun E.,
Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
A Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Theng S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhong K., Zho C., Zhon M., Zhang G., Zhao O., Zheng L.,
RA Chobs R.A., Myers E.W., Rubin G. M., Venter J.C.;
Schence 287:2185-2195(2000).
Schence 287:2185-2195(2000).
Schence 287:2185-2195(2000).
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Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Addans M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeilffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Banos P.V., Bernan B.P., Bhandari D., Boishakov S., Beckova D., Botchan M.R., Bouck J., Brokstein P., Brothan B.R., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.0%; Score 47; DB 5; Length 259; 80.0%; Pred. No. 0.46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28373 MW; 13249A284038F4F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flyase; FBGN035666; CG6580.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Scr_procease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00020; Tryp_SPS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
PHYdrolase; Setline procease.
SEQUENCE 259 AA; 28373 MW; 13249A284(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003564; AAF50712.1; -. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SER6 protein (RE66795p).
SER6 OR CG2071.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 CSGDSGGPLV 214
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de Pablos B.; Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Dodson K., Doup L.E.; Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

A Durbin K.J., Evangelista C.C., Ferrara C., Ferriera S., Fleischmann W.,

Ra Fosler C., Gabriellan A.E., Garrell J.H., Gu Z., Guan P., Harris M.,

A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Blouck J.,

Ra Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Blouck J.,

Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Ra Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Ra Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Ra Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

An Martei B., McIntosh T.C., McGeod M.P., McPherson D.,

Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Ra Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Ra Reinert K., Saden Kiamos I., Simpson M., Skupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Ra Stirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Rang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Rang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Rang X.A., Myers E.W., Rubin G.M., Venter J.C.;

Rang X.A., Myers E.W., Rubin G.M., Venter J.C.;

Rang X.A., Myers E.W., Rubin G.M., Venter J.C.;

Rangence 287:2185-2195(2000)
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00722; CHYMOTRTPSIN.
SMART; SM00020; TIYP_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
HYGYOLASE; SETINE PICTERASE.
HYGYOLASE; SETINE PICTERASE.
SEQUENCE 259 AA; 28078 MW; 49D5EB6E37A9D4DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
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Eukaryota; Metazoa; Arthropoda; Trac
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EMBL; AE003569; AAF50872.1; -.
EMBL; AX089642; AAL90380.1; -.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0011834; Ser6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG1304 protein (RE14171p). CG1304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BERKELEY;
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Matches
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Q9VRD1
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Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
A brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pétélfére B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pétélfére B.D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
R. Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
R. Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
R. Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
R. Burtis R.C., Busam D.A., Butler H., Cadleu E., Davies P.,
A cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
A charle B.D., Delcher A., Davies M., Davies P.,
Burtis R.C., Gabriellan A.E., Gary N.S., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Bestin D., Houston K.A., Howland T.J., Weil M.-H., Ibegwam C.,
Adali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum K.A.,
Liu X., Mattel B., McIntosh T.C., Kraft C., Kravitz S., Kulp D., Lia Z.,
Liu X., Mattel B., McIntosh T.C., Morison D.E.,
Aberkulov G., Milshima N.V., Mobrary C., Morriss J., Moshrefi A.,
Rhount S.M., Moy M., Murphy B., Murphy L., Muruny D.M., Nelson D.L.,
Rhount S.M., Moy M., Murphy B., Murphy L., Wuruny D.M., Nelson D.K.,
Rhount S.M., Woodage T., Shapson M., Strong R., Sun E.,
Shele E., Spradling A.C., Slapler C., Stapleton M., Strong R., Wannary B.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A,
R., The genome sequence of Drosophila melanogaster F.,
Shenc S., Shangary C., Stander S., Shangary S.,
Shangary S.H., Nyers E.W., Kubin G.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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PROSITE; PS00134; TRYPSIN_HIS; 1.
HQTCOlase; Serine profease,
SEQUENCE: 260 AA; 27860 MW; 0933B34BF20A7675 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 5;
Pred. No. 0.46;
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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InterPro; IRR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                 MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRYPSIN FAMILY.
EMBL; AE003569; AAF50871.1; -.
EMBL; AY095196; AAM12289.1; -.
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                       SEQUENCE FROM N.A.
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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                       Addans M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Addans M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Addans M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., Gacore R.A., Levis S.E., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gacore R.A., Levis S.E., Scherer S.G., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandreal, M.D., Zhang Q., Cham L.X., Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G., Marn K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Marn K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Marn K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Marn K.H., Beasley E.M., Beacson K.Y., Benos P.V., Bernadal W., Baxendale J., Bayaktaroglu L., Beasley E.M., Berkov D., Botcher M., Bouck J., Brokstein P., Burttis R.C., Busam D.A., Buttler H., Cadleu E., Center A., Chandra I., Marts R.C., Busam D.A., Buttler H., Cadleu E., Center A., Chandra I., And Pabloson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Murtis R.J., Evangelista C.C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Golder A., Goorg F., Gorrell J.H., Gu Z., Gunn P., Harris M.L., Harvey D., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Wei M. H., Ibeywam C., Jalali M., Kalush F., Karpen G.H., Kee Z., Kennison J.A., Ketchum R.A., Jalali M., Kalush F., McIntcoh H.P., McIncoh H.P., McIncoh
                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCIENCE 287:2185-2195(2000).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
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                                                                                                                                            01-MAY-2000 (TrEMBLrel, 13, 01-MAY-2000 (TrEMBLrel, 13, 01-JUN-2002 (TrEMBLrel, 21, CG10475 protein.
                                                                                                                 PRELIMINARY;
                  1 CXGDSGGPXV 10
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"Isolation and cloning of Ser4, a gene encoding a trypsin-like serine protease in Drosophila melanogaster.";
Blochim. Biophys. Acta 1395:141-144(1998).
EMBL; AF006639; AAC14351.1; --
HSSP; P20231; 1AAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease SER4 precursor.
SER4 OR CG8867.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petergota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Flerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                     Gaps
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                                                                                     Score 47; DB 5; Length 262;
Pred. No. 0.46;
0; Mismatches 2; Indels
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1 21 POTENTIAL.
CHAIN 37 265 ACTIVE SERINE PROTEASE SER4.
SEQUENCE 265 AA; 28950 MW, 551A92CDE2E28BC8 CRC64;
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
SEQUENCE 262 AA; 28511 MW; 7F0F3F66044082CA CRC64;
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Last sequence update)
Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; tryps.in; 1.
SMART; SMO0200; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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                                                                                         94.08;
                                                                                                            80.08;
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                                                                                  Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                    208 CSGDSGGPLV 217
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SER4 OR CG8867
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94.0%;
80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                           NCBI_TaxID-7165;
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RA Adams M.D., Celniker S.E., Li P.W., Fvans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Fvans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Li P.W., Hoskins R.A., Galle R.F.,
Raranden R.C., Regers Y.-H.C., Blazel R.G., Champer M., Flerifer B.D.,
RA Brill J.F., Aphayani A., An H.-J., Andrews-Fennikoch C., Baldwin D.,
RA Ballaw R.M., Basuu A., Bernan B.P., Bhandari D., Belshakov S.,
Ballew R.M., Basuu A., Bernan B.P., Bhandari D., Bolshakov S.,
Ballew R.M., Cavley S., Dalike C., Davenbort L.B., Davies P.M.,
Borkova D., Botchan M.R., Buller H., Cadteu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Buller H., Cadteu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Buller H., Cadteu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Buller H., Cadteu E., Center A., Chandra I.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrat B., Davies P.C., Dunn P.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Berrina B., Coller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Kenlison J.A., Ketchum R.A.,
RA Hartis N.L., Harvey D., Halman T.J., Herrandez J.R., Fariandez J.R.,
RA Liu X., Mattel B., McIntosh T.C., Mortis J., Moshrefi A.,
RA Liu X., Mattel B., McIntosh T.C., Mortis J., Moshrefi A.,
RA Liu X., Mattel B., McIntosh T.C., Mortis J., Moshrefi A.,
Rabon D.R. Woy M., Pully B., Murphy L., Muzny D.M., Nelson D.L.
Rabon D.R., Woy M., Wurphy B., Murphy L., Muzny D.M., Nelson D.K.,
Rabon D.R., Woy M., Wurphy B., Murphy L., Muzny D.M., Nelson R.,
Spier E., Spradling A.C., Pan S., Pollator E., Wang A.H., Wang X.,
Rabon D.R., Woyen E., Wassarman D.A., Weller E., Wang A.H., Wang Z.-Y., Wassarman D.A., Weller D.C., Scheeler F., Shen R.,
Rabon D.R., Woyen E., Zaveri J.S., Zhou S., Zhu S., Z
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001354; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00135; TRYPSIN_ERR; 1.
Hydrolase; Serine protease.
SEQUENCE 266 AA; 28720 MW; 92A7E303271B2AF8 CRC64;
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Last annotation update)
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                  MEDLINE-20196006; PubMed-10731132;
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02,
21,
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Matches 8; Conservative
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01-FEB-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Serine protease.
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Q17030;
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Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
A manatides P.G., Scherer S.E., Il P.W., Hoskins R.A., Galle R.F.,
A charles R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A shiton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Black G., Nelson C.R., Miklos G.L.G.,
An R.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A Blalew R.M., Baus A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Blothakov S.,
Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenpbrt L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleisschmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gulan P., Harris M.,
RA Barris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SETALINE-31; TISSUE-MIDGUT;
MEDLINE-97075119; PubMed-8917545;
Dimopoulos G.M., Richman A., della Torre A., Kafatos F.C., Louis C.;
Dimopoulos G.M., Richman A., della Torre A., Kafatos F.C., Louis C.;
"Identification and characterization of differentially expressed cDNAs of the vector mosquito, Anopheles gamblase.",
Proc. Natl. Acad. Sci. U.S.A. 93:13066-13071(1996).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE FEMEL; Z69978; CAA93818.1; --
HSSP: P00763; IDPO.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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InterPro; IPR001354; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
Prints, Pr00725; CHYMOTRYSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LOM; 1.
PROSITE; PS00134; TRYPSIN_LSER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 268 AA; 29176 MW; 7BEE8462EFIFD8BE CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pred. No. 0.47;
0; Mismatches
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Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Liargy Y., Lin X., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mentkov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mentkov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Nelson D.R., Nelson R.A., Nivon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Shen B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E., Shen H., Sale E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Sylskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang G., Zheng L., Zhong K.H., Zhong W., Zhu S., Zhu X., Smith H.O., Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E. George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Mizanda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S. Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.
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Pred. No. 0.48;
0; Mismatches 2; Indels
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SEQUENCE 271 Aa; 29814 MW; 0A410C925CBE8826 CRC64;
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SOSTE; PS50240; TRYPSIN_DOM; 1.
ROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
ROSITE; PS00135; TRYPSIN_SER; 1.
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IPR001254; Ser_protease_Try
089; trypsin; 1.
00722; CHYMOTRYPSIN.
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Best Local Similarity 80.0%,
Best Local 8; Conservative
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Search completed: May 12, 2003, 15:38:40 Job time: 24.6 secs

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Scoring table:

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2210c
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                                                                                                                                                                             May 12, 2003, 15:31:22; Search time 11.44 Seconds (without alignments) 46.591 Million cell updates/sec
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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2DS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT
/s1DS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT
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                      GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AAR04871
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Gapop 10.0 , Gapext 0.5
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                       AAE20157
ID AAE
                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acute and chronic inflammation and infections caused by viruses or microorganisms. The diagnostic kits are useful for the detection of these illnesses and for the detection of the transport molecule and/or its distribution in vivo. The ligands have excellent solubility in the medium at the site of action and are easy and inexpensive to covert into AABB6643-AABB6920 represent peptides used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel ligands which bind to transport molecules, comprising a therapeutic and/or diagnostic agent (A) non-covalently bonded via a linkage cleavable in vivo depending on pH and/or enzymatically with a substance (B) having an association constant KA to a transport molecule of above 10^3 M^-^1, is new. The medicaments are especially useful for the treatment of cancers, autoimmune diseases,
                                                                                                                                                                                                          Gaps
                                           The sequences given in AAR25311-19 are cyclic peptides which act as contact inhibitors of animal cells. They are resistant to decomposition by Mydrolytic enzymes and can be maintained at high lavels of activity for a long period in vivo. The peptides are cyclic and may have 1-16 pref. 1-4 amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transport molecule; ligand; cancer treatment; autoimmune disease; inflammation; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New ligand, comprising therapeutic or diagnostic agent bonded non-covalently with substance having high affinity to transport
                                                                                                                                                                                                        ö
                                                                                                                                                                         Length 4;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Transport molecule/ligand binding-associated peptide #5.
                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0;
              Disclosure; Page 3; 6pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 39; 74pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KTBT-) KTB TUMORFORSCHUNGS GMBH.
                                                                                                                                                                                                                                                                                                                                                AAB86859 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-2001; 2001WO-EP02833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-2000; 2000DE-1012120
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-589998/66.
                                                                                                                                           4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200168142-A1.
                                                                                                                                                                                                                                                        1 RGDA 4
                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-2001
                                                                                                                                                                                                                                      1 RGDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                AAB86859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kratz F;
                                                                                                                                                                                                                                                                                                               RESULT 2
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DB 22; Length 4;

100.0%; Score 21;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stimulating growth and repair of cartilage, useful for treating e.g. arthritis, by local administration of an agonist of non-proteolytically activated thrombin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of stimulating growth and repair of cartilage. The method involves administering to the site, an agonist of non-protecolytically activated thronin receptor (WRAR). The method is used in human or veterinary medicine for the treatment of arthritic joints and damage/loss of cartilage caused by traumatic injury. Also chondrocytes may be cultured in presence of NPAR agonist to provide cells for implantation at sites requiring growth/repair of cartilage. The present sequence is human thrombin peptide. The derivatives of thrombin peptide which serves as a NPAR agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cartilage growth, cartilage repair; arthritic joint; traumatic injury; non-proteolytically activated thrombin receptor; NPAR; chondrocyte; therapy; implantation; thrombin peptide; human.
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bergmann J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 23;
llarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
                  Pred. No. 7.8
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stlernberg J,
100.08; Pr
                                                                                                                                                                                                                                                                           AAE20157 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 25; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU78374 standard; Peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2001; 2001WO-US22668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-2000; 2000US-219800P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carney DH, Crowther RS,
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human thrombin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-268953/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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ID AAU
XX
AC AAU
XX
DT 18-
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Carney DH,

Synthetic.

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The present sequence is that of a thrombin receptor binding domain peptide that is used in a claimed method for promoting cardiac peptide that is used in a claimed method for promoting cardiac trissue repair. The method involves administering an angiogenic thrombin derived peptide. The peptide comparises the present thrombin receptor binding domain together with a scrine esterase conserved sequence (see AAM50857), or preferably a peptide (see AAM50858) which includes both these sequences. The thrombin-derived peptide is administered during or following cardiac surgery by injection into cardiac tissue, and may be formulated as a sustained release formulation. It is used in claimed methods of stimulating revascularisation, stimulating vascular nedothelial cell creatency inhibiting vascular occlusion, and inhibiting restencial peptide may be coated onto the catheter.
                                                                                                                                                 Promoting cardiac tissue repair, stimulating revascularisation, stimulating vascular endothelial cell proliferation, and inhibiting vascular occlusion by using anglogenic thrombin derivative peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAR24514-8 are peptides which are useful as platelet antagonists. These peptides have higher activity than the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide(s) comprising arginine-glycine-asparagine and hyaluronic acid - useful as platelet antagonists with higher activity than arginine-glycine-asparagine-valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 21; DB 23;
100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 5; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR24517 standard; Protein; 5 AA
                                                                                                                                                                                                                                    Claim 2; Page 19; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Platelet antagonist pepetide 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SEGK ) SEIKAGAKU KOGYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90JP-0253849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clinical effect; antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90JP-0253849,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry).
                      (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-204525/25.
                                                                                                       WPI; 2002-179665/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                 Carney DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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AAR24517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a method of stimulating bone growth at a site in a subject in need of osteoinduction. The method involves administering an agonist to stimulate bone growth at a site in a subject (e.g. a farm animal, companion animal or laboratory animal), in need of osteoinduction, such as the site in need of a bone graft in a subject, a segmental bone gap, a bone void or a non-union fracture. This sequence represents a thrombin peptide derivative obtained from a serine esterase that can stimulate or activate the non-proteolytically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stimulating bone growth at a site in a subject in need of osteoinduction, such as a site of bone graft, segmental bone gap, bone vold or non-union structure, by administering agonist of activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombin receptor binding domain; thrombin; revascularisation; vascular occlusion; tissue repair; vulnerary; vasotropic; cardiant; angiogenesis; restenosis; therapy; human.
                                          Thrombin; osteopathic; receptor; agonist; bone growth stimulation; osteoinduction; farm animal; companion animal; laboratory animal; bone graft; segmental bone gap; bone void; non-union fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombin receptor binding domain used for cardiac tissue repair
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                                                                                                                                                                                                                                                                                                                                                                                           Redin WR;
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100.0%; Pred. No. 7.8e+05;
11ve 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                        Yang
                                                                                                                                                                                                                                                                                                                                                                                           Simmons DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM50856 standard; Peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 22; 27pp; English.
Thrombin peptide derivative #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUL-2001; 2001WO-US21944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUL-2000; 2000US-217583P.
                                                                                                                                                                                                                                                             18-JUL-2001; 2001WO-US22641.
                                                                                                                                                                                                                                                                                                     19-JUL-2000; 2000US-219300P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activated thrombin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Crowther RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-303796/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
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                                                                                                                                                                          WO200205836-A2.
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RGDA 4

Matches

Sequence

1 RGDA

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RESULT 5 AAM50856 AAM50856;

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Gaps

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Length 4; Indels us-09-909-348-3.rag

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09-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                            (THRO-) THROMGEN INC.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stent placement
                                                                                                                                                                            WO200112656-A1
                                                                                                                                                                                                                                                               L7-AUG-1999;
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                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US4879237-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                             activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthetic.
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    AAB72600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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      human immunodeficiency virus (HIV) by treating the virus, or its target cell, with a thrombospondin or thrombospondin analogue. Thrombospondin blocks binding of HIV to its cellular receptors. Thrombospondin or its analogues can used to prevent infection by HIV, in both contraceptive and non-contraceptive compositions/devices. They are already known to reduce infectivity of some bacteria and protozoa. The present sequence represents a human thrombospondin-1 type III repeat peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for suppressing infectivity of human immunodeficiency virus (HIV) by treating the virus, or its target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                       Gaps
conventional peptide of Arg-Gly-Asp-Val. These peptides have a clinical effect at a lower dose, dosage is 2.5-5.0 mg/kg/day.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                Human; thrombospondin; HIV; infection; inhibition; chemokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5;
                                                                           Length 5;
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                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suppressing infectivity of human immune deficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 21; DB 20;
100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                                                                         Score 21; DB 13;
Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                    Human thrombospondin-1 type III repeat peptide.
                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nachman RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 33; 67pp; English.
                                                                                                                                                                                                                              AAY17781 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB72600 standard; Peptide; 5 AA
                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORR ) CORNELL RES FOUND INC
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97US-0066294.
                                                                                                      Conservative
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Best Local Similarity
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                                                                        Query Match
Best Local Similarity
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                                           5 AA;
                                                                                                                                                                                                                                                                                                                                                                 contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9926649-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-1998;
25-NOV-1997;
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2 RGDA 5
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RGDA 5
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                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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Matches
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The present invention relates to a method for inhibiting thrombin cartivation in a human cell expressing protease activated receptor 1 (PARI). The method involves using peptides (e.g. the present peptide) that inhibit platelet activation. The method is useful for preventing thrombosis and platelet aggregation. The method can be used for patients with acute coronary syndromes (e.g. cresende anglan, myccardial infarction) and for individuals who have acute coronary syndromes and receive percutaneous transluminal coronary angioplasty with an artificle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activated receptor 1 (PAR1), comprises contacting mixtures of thrombi
and human cell expressing PAR1, with a peptide that inhibits platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                   Platelet aggragation inhibitor; thrombin activation inhibitor; protease activated receptor 1; PARI; platelet activation inhibitor; thrombosis; acute coronary syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting thrombin activation in human cell expressing
Thrombin-induced platelet activator antagonist #39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR04871 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                     17-AUG-2000; 2000WO-US40669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmater AH, Hasan AAK;
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Query Match
Best Local Similarity
Matches 4; Conserv
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2 RGDA 5
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                                                                                                                                                  1 RGDA
                                                                                               Sequence
                                                                                                                                                                                                                               ABP48385;
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                                                                             Synthetic peptide(s) from fibronectin- used in control of cell attachment
                                                                                                                     This polypeptide mediates the attachment of animal cells to substrates. The substrate (I) is contacted with cells and with a soln. contg. this polypeptide. This attachment can be prevented in addition to detaching the cells from (I) once attached. Applications are in eg fermentation, cell line prepn., diagnosis and therapy.
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The peptide, or shorter versions contg. the RGD active site from fibronectin, can be used to prevent and reverse attachment of cells to substrates. This can be used in cell prodn., fermentation, cell line prepn., cell matrix prodn., diagnostics and therapy. The
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                                                                                                                                                                                           100.0%; - Score 21; DB 11; Length 6; 100.0%; Pred. No. 7.8e+05; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide(s) contg. arginine-glycine-aspartic acid sequence to prevent and reverse cell attachment or to promote cell
                                           Pierschbacher MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruoslahti EI, Hayman EG, Pierschbacher MD;
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 2..4
                                                                                                                                                                                                                                                                                                                                             Cell attachment promoting peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 8; 12pp; English.
                                                                                                                                                                                                                                                                                          AAR11506 standard; Protein; 6 AA.
                                                                                                       Claim 1; page 10; 13pp; English
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85US-0738078.
        890S-0738078
                         (JOLL-) LA JOLLA CANCER RES.
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                                           Hayman EG,
                                                                                                                                                                                                                                                                                                                            12-JUN-1991 (first entry)
                                                                                                                                                                                                             Conservative
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                                                           WPI; 1990-154405/20.
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                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                           6 AA;
                                                                                      and detachment
                                          Ruoslahti EI,
       24-MAY-1989;
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24-MAY-1985;
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Active-site
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) a target site, comprising a first (FI), a second (F2), and a third (F3) target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) (C1) a polynuclectide (III) encoding (I) or (III); and (I) (I) involves selecting the F1 zinc finger such that (I) thinds to the S1 target subsite, and selecting the F2 zinc finger such (I) that binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, and selecting the F2 zinc finger such that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite (I) is useful in studying gene function, and for human therapeutics and plant engineering (I) (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
peptide can be used for eg mobilisation of bone marrow cells; prevention and reversal of attachment of disseminated tumour cells locally such as in the case of an operation performed in the peritonal cavity, to prevent adhesions and scar formations locally as binding to epithelial cells of the urinary tract or intestine, diagnosis and treatment of E. coli related infections, and identification of various pathogenic bacterial strains. The peptide is pref. prepd. by solid phase synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zinc finger protein; ZFP; DNA binding protein; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 12; 100.0%; Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP48385 standard; Peptide; 7 AA.
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a target site, comprising a first (FI), and a third (FI) and a third (FI) and a third (FI) and a third (FI) and a third (FI).

In finger, ordered FI, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (SI), a second (S2), and a third (SI) target subsite. Also described are: (I) a polypeptide (II) encoding (I) or (II); and (II) ends to the SI target subsite, selecting the F2 zinc finger such that to binds to the SI target subsite, and selecting the F3 zinc finger such that it binds to the SI target subsite, and selecting the F3 zinc finger such that it binds to the SI target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therefore the expression of a target region within a subject; in diagnostic methods for sequence specific detection of target uncleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity
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a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. AB071213 to AB072214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention describes a zinc finger protein (I) that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
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                                                                                                                                                                                                                     100.0%; Score 21; DB 23; Length 7; llarity 100.0%; Pred. No. 7.8e+05; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc finger protein related peptide motif SEQ ID NO:670.
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Matches 4; Conserv
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Synthetic.
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The present invention describes a zinc linyer process.

The present invention describes a zinc linyer process.

The present invention describes a zinc describe that the comprises, in 3'-5' direction, a first (S1), and a third (F3) and a third (S3) target subsite. Also described are: (1) a polypeptide (I) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that It binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, and selecting the farile to that binds to a target site. (I) is useful in studying gene function, and for human to therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequences specific detection of the compensation of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced to represent DNA target sequences and zinc finger peptides which are given represent DNA target sequences and zinc finger peptides which are given
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and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ7214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zinc finger protein; ZFP; DNA binding protein; zinc finger
                                                                                                                                         Length 7;
                                                                                                                                                                               Indels
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                                                                                                                                     100.0%; Score 21; DB 23;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                               ABP48597 standard; Peptide; 7 AA.
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                                                                                                                                                                               4; Conservative
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                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) is target site, comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) encoding (I) or (II); and a third (S3) target subsite. Also described are: (I) a polypeptide (II) encoding (I) or (II); and (S1) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S2 target subsite, alecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc (I) at that it binds to the S2 target subsite, and selecting the F3 zinc that binds to a target subsite, (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human charapeutics and plant engineering. (I), (II) or (III) is useful in the charapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods and in assays to determined the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phenotype and function of gene expression. (1) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New zinc finger protein that binds to target site, useful in stugene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc finger protein; 2FP; DNA binding protein; zinc finger.
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Pred. No. 7.8e+05;
                                                                                                               Indels
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                                     Score 21; DB 23;
Pred. No. 7.8e+05;
Mismatches 0;
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100.0%;
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Best Local Similarity luv...
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                                                                                                                                                 Length 7;
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                                                                                                                                             100.0%; Score 21; DB 23; 100.0%; Pred. No. 7.8e+05;
in the exemplification of the present invention
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                                                                                                                                                                               Best_Local Similarity 100.
Matches 4; Conservative
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Marches 4; conservative 0; mismarches 0; indels 0; Gaps		Search completed: May 12, 2003, 15:36:04 Job time : 12.44 secs
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Appl Appl Appli Appli

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Sequence 2, Appli
Sequence 8, Appli
Patent No. 5196510
Sequence 20, Appl
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5196510
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Sequence 50,
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Sequence 2, A
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Sequence 2
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Sequence 5
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APPLICANT: Lan, Jianging
APPLICANT: Shih, PoJen
APPLICANT: Shifferli, Revin P.
TITLE OF INVENTION: Peptide-Enhanced Cationic Lipid
TITLE OF INVENTION: Transfections
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: RC-LUDS/MS-LUDS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,130
FILING DATE: 04-JUN-1996
CLASSIFICATION NUMBER: US 08/477,354
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CATULHERS, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/POCKET NUMBER: 32-95A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
US-08-480-367B-20
US-08-487-221A-20
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/08658130 Patent No. 5736392 GENERAL INFORMATION:
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not relevant
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; HYPOTHETICAL;
; FRAGMENT TYPE:
US-08-658-130-19
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Patent No. 535266
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30.649 Million cell updates/sec
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Sequence 1
Sequence 4
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                       GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-644-660-85
US-07-602-847C-1
US-07-139-7624-100
US-09-139-762A-113
US-09-139-762A-113
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US-08-482-085B-35
US-08-475-411A-14
US-08-478-029A-14
US-09-444-791A-35
US-08-981-088-4
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US-07-602-847C-9
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US-09-426-680-2
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indela
                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08723
FILING DATE: 04-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION UNBER: US 08/477,354
RILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5352664-2; Patent No. 5352664
; Patent No. 5352664
; APPLICANT: Carney, Darrell H.; Glenn, Kevin C.
; TILLE OF INVENTION: THROWBIN DERIVED POLYPEPTIDES; COMPOSITIONS AND METHODS FOR USE
                                                5: Greenlee, Winner and Sullivan, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 3295A WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/925,201
FILING DATE: 31-OCT-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-08-232-081B-3
; Sequence 3, Application US/08232081B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080.
TELEPAX: (303) 499-8089
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  internal
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                               STATE: Colorado
                                                                                       Boulder
                                                                                                                              COUNTRY: U
                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:2:
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      Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,780A,
FILING DATE: 16-Mar.198
                                                                                                                                                                                                                                                                                                                                        SHIH, POJEN
JESSE, JOBL A.
SCHIFFERLI, KEVIN P.
GEBEYEHU, GULLLAT
INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Life Technologies, Inc.
TITLE OF INVENTION: Peptide-Enhanced Cationic Lipid
TITLE OF INVENTION: Transfections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: GREENLEE, WINNER & SULLIVAN STREET: 5370 MANHATTAN CIRCLE, SUITE 201 CITY: BOULDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 21; DB 4; Best Local Similarity 100.0%; Pred. No. 2e+05; Matches 4; Conservative 0; Mismatches 0
    Score 21; DB 1;
Pred. No. 2e+05;
                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 32-95C TELECOMMUNICATION INFORMATION: TELEPHONE: (303)499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 23: US-09-039-780A-23
                                                                                                                                                                                                                               Sequence 23, Application US/09039780A
Patent No. 6376248
GENERAL INFORMATION:
APPLICANT: HAWLEY NELSON, PAMELA
LAN, JIANOING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: SULLIVAN, SALLY A.
REGISTRATION NUMBER: 32,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application PC/TUS9608723
GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (303 499-8089 INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
  h 100.0%;
Similarity 100.0%;
4; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11near
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
PCT-US96-08723-19
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US-09-039-780A-23
                                                                                     1 RGDA 4
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                                                                                                                            1 RGDA
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APPLICANT: Lazarus, Robert A.,
APPLICANT: Lazarus, Robert A.,
APPLICANT: Seymour, Jana I.
TITLE OF INVENTION: No. 5227469el Platelet Aggregation Inhibitors From The Leec
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Genented. Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Jana L.
No. 5227469el Platelet Aggregation Inhibitors From The Leec
                                             Gaps
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  Length 9;
  100.0%; Score 21; DB 4; 100.0%; Pred. No. 2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: patin (Genentch)
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/602,847C
FILING DATE: 19901026
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/479,829
FILING DATE: 14-FEB-1990
ATTORNEY/AEBWI INFORMATION:
NAME: Winter, Daryl B.
REGISTRATION NUMBER: 32,637
                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: Genentech, Inc.
1: 460 Point San Bruno Blvd
South San Francisco
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/07602847C Patent No. 5227469
                                                                                                                                                                                                                                          Sequence 1, Application US/07602847C Patent No. 5227469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Leazurus, Robert A.,
APPLICANT: Seymour, Jane L.
TITLE OF INVENTION: NO. 522746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 60 ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
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                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMINO ACID
Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY:
US-07-602-847C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Sou
STATE: Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGDA 4
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                                                                                       1 RGDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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APPLICAMT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: OVEREXPRESSED in Carcinomas
TITLE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: U5/09/644,600
CURRENT FILING DATE: 1998-23
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR APPLICATION NUMBER: 09/027,337
PRIOR FILING DATE: 1998-02-00
PRIOR FILING DATE: 1998-02-20
PRIOR FILING DATE: 1998-02-20
SEQ ID NO 85
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Residues 248-256 of the TADG-15 protein US-09-644-600-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,081B
                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 70
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21; DB 2;
Pred. No. 2e+05;
                                    APPLICANT: GOMI, HIDERUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: NGGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22040-0747
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 85, Application US/09644600 Patent No. 6451500 GENERAL INFORMATION:
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Best Local Similarity 100.0%; P
Matches 4; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SYENSSON, LEBONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-644-600-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-232-081B-3
                                                                                                                                                                                                                     CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                          Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pillsbury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 0.2-UN-1997
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
INFORMATION FOR SEO ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid
STANDENNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 113, Application US/09139762A
Patent No. 6013453
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: GB 9416880.4
20-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                        18-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 20-AUG-19:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-139-762A-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C. COUNTRY: USA ZIP: 20005-3918
                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-139-762A-113
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Patent No. 6013453
GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
APPLICANT: Bunchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 21; DB 1; Length 10; 100.0%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pillsbury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W. CITY: Washington
                                                                                                         COMPUTER: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                           SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/602,847C
FILING DATE: 19901026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-JUN-1997
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
                                                                                                                                                                                                                      APPLICATION.

FILING DATE: 19901020
CLASSIFICATION: 435
FRICA APPLICATION DATA:
APPLICATION NUMBER: 07/479,829
FILING DATE: 14-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: WINTER, DATYL B.
REGISTRATION NUMBER: 32,637
REPERRENCE/DOCKET NUMBER: 667
TELECOMMUNICATION INFORMATION:
""TEPHONE: 415/266-1249
: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPALANCE OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS OPERATINES: WOR'D PERFECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 10 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
                                        California
                                                                               94080
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APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W
TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
NUMBER OF SEQUENCES: 112
No. 5770697el Peptides Comprising Repetitive Units of Amino Acids and DNA Sequences Encoding the Same
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                                         NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flahr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DUS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,509B
FILING DATE: 07-JUN-1995
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OFT-1987
FILING DATE: 1900-1987
FILING DATE: 104-000-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,049
ATTORNEY/AGENT INFORMATION:
NAME: TRECARTIN NUMBER: 31,049
ATTORNEY/AGENT INFORMATION:
NAME: TRECARTIN NUMBER: 31,049
ATTORNEY/AGENT INFORMATION:
NAME: TRECARTIN NUMBER: 31,049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 21; DB 1; 100.0%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK PELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
TELEPHOX: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Chambers, James
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferrari, Franco A.
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Pollock, Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 11 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                      STREET: Four Embarca
CITY: San Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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Matches 4; Conserv
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US-08-482-085B-35
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APPLICANT:
APPLICANT:
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Pred. No. 39;
); Mismatches 0; Indels
                                                                                     Length 10;
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TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Sulte 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111

ZIP: 94111

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,716
FILING DATE: 06-NOV-1990
                                                                              100.0%; Score 21; DB 3;
100.0%; Pred. No. 35;
1ve 0; Mismatches (
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                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/07609716
Patent No. 5514581
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: ROWLand, Bertram I
REGISTATION NUMBER: 20015
REFRENCE/DOCKET NUMBER: A-5:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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INFORMATION FOR SEQ ID NO: 14:
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100.0%;
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Crissman, John w
Dorman, Mary A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-139-762A-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-609-716-14
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Best Local Similarity
Matches 4; Conserv
                                                                                                      Best Local Similarity
Matches 4; Conserv
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RGDA 8
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APPLICANT:
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US-07-609-716-14
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APPLICANT:
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                                                                                     Query Match
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STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ferrati, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,029A FILING TOO JUN-1995 CLASSIFICATION: 435
                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING APPLICATION NUMBER: US 06/927,258
FILING APPLICATION NUMBER: US 06/927,258
FILING APPLICATION NUMBER: US 06/927,258
TELENGY AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REGISTRATION NUMBER: A-55186-9/RFT/MIK
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609,716
FILING DATE: 06 NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
              MABER: US/08/475,411A
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08478029A Patent No. 6184348 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity luv...
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid.
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-475-411A-14
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US-08-478-029A-14
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Patent No. 6140072
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF ENVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,085B
FILING DATE: US-JUN-1995
CLASSIFICATION: 435
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PatentIn Release #1.0, Version #1.30
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Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION NUMBER: US 08/15,155
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~wommatible
                                                                                                                                                      COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-482-085B-35
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Four CITY: San Francisco
                         San Francisco
                                            California
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SOFTWARE: Patenti
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Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                               OPERATING SYSTEM:
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STRANDEDNESS: si
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Gaps

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PRIOR APPLICATION DATA:

APPLICATION WHERE: US 07/114,618
FILING DATE: 29-CCT-1987
FILING DATE: 29-CCT-1987

PRIOR APPLICATION MUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: TECENTIAL, RICHARG F.
REFERENCE/DOCKETY NUMBER: A 55186-8/RFT/ATK
TELECOMMUNICATION INFORMATION: 14:
TELEPHONE: 415-781-1989
TELERA: 415-398-3249
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CERRACTERISTICS: LENGTH: 11 annio acids
TYPE: peptide
US-08-478-029A-14
OUBET WALCH
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OUBET WALCH
US-08-478-029A-14

OUBET WALCH
US-08-47
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RESULT 2
US-10-050-611-1
; Sequence 1, Application US/10050611
; Publication No. US20020187933A1
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Best Local Similarity
Matches 4; Conserv
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                                                                                                   (without alignments)
47.436 Million cell updates/sec
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Sequence 671,
Sequence 672,
Sequence 672,
Sequence 673,
Sequence 674,
Sequence 674,
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Sequence 3,
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Sequence 3,
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Sequence 3,
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Sequence
Sequence
Sequence
                                                                                    May 12, 2003, 15:38:52 ; Search time 7.76 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-050-688-3
US-09-911-569-23
US-09-909-348-3
US-09-909-122-3
US-09-909-122-3
US-09-990-186-289
US-09-990-186-671
US-09-990-186-673
US-09-990-186-673
US-09-990-186-673
US-09-990-186-673
US-09-990-186-675
US-09-990-186-675
US-09-990-186-696
US-09-990-186-696
US-09-990-186-696
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US-09-990-186-1048
                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameter's:
                                                                                                                                                                                                                                                  349150 seqs, 92025710 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        protein search, using sw model
                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                             US-09-909-348-3
21
1 RGDA 4
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                                                                                                                                                              Perfect score:
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                                                        OM protein
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                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                     Run on:
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No.
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Sequence 2716, Sequence 234, Sequence 3177, Sequence 31702, Sequence 3702, Sequence 3702, Sequence 3749, Sequence 670, Sequence 
                                                                                 Sequence 1928,
Sequence 1961,
Sequence 1989,
Sequence 1990,
Sequence 1996,
                                                                                                                                                                                                1997
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                                              Sequence Sequence
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Sequence
Sequence
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                                                                              US-09-990-186-1928
US-09-990-186-1961
US-09-990-186-1999
US-09-990-186-1999
US-09-990-186-1997
US-09-990-186-2007
US-09-990-186-2014
US-09-990-186-2014
US-09-990-186-3169
US-09-990-186-3177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-989-789-671
US-09-989-789-672
US-09-989-789-673
US-09-989-789-674
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US-09-989-789-670
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ALIGNMENTS

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Gaps
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Sequence 3, Application US/10050692
| Sequence 3, Application US/10050692
| Publication No. US20020182205a1
| GENERAL INFORMATION:
| APPLICANT: Carney, Darrell H.
| APPLICANT: Crowther, Roger S.
| APPLICANT: Simmons, David J.
| APPLICANT: Fang, Jinping
| APPLICANT: Redin, William R.
| TILLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN TITLE OF INVENTION: MUBBER: US/10/050,692
| CURRENT FILING DATE: 2002-01-16
| PRIOR APPLICATION NUMBER: 09/909,122
| PRIOR APPLICATION NUMBER: 09/909,122
| PRIOR ELLING DATE: 2000-07-19
| PRIOR FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 9; Length 4; llarity 100.0%; Pred. No. 3.1e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: fragment of human prothrombin US-10-050-692-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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APPLICANT: HAWLEY-NELSON, PAMELA
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                 ZIP: 80303
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                CITY: BOULDER
                                                                                                                                                                                                                                    COUNTRY:
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                            TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED TITLE OF INVENTION: PEPTIDES FILE REFERENCE: 3033.1000-000 CURRENT APPLICATION NUMBER: US/10/050,611 CURRENT FILING DATE: 2002-01-16 PRIOR APPLICATION NUMBER: 09/904,090 PRIOR FILING DATE: 2001-07-12 PRIOR APPLICATION NUMBER: 60/217,583 PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                              Length 4;
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llarity 100.0%; Pred. No. 3.1e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 21; DB 9; 100.0%; Pred. No. 3.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: peptide fragment of thrombin US-10-050-688-3
                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: human fragment of thrombin US-10-050-611-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,348
PRIOR FILING DATE: 2001-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/219,800 PRIOR FILING DATE: 2000-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/09911569 Publication No. US20030069173A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/10050688 Publication No. US20020198154A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Thes 4; Conserve
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: Carney, Darrell H.
APPLICANT: Carney, Darrell H.
APPLICANT: Crowther, Roger S.
APPLICANT: Stlennberg, Janet
APPLICANT: Bergmann, John
TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin
FILE REPERENCE: 3033.1003-001
CURRENT APPLICATION NUMBER: US/09/909,348
CURRENT FILING DATE: 2001-07-19
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                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
GEBEYEHU, GULILAT
TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
                                                                                                            ADDRESSEE: GREENLEE, WINNER & SULLIVAN
STREET: 5370 MANHATTAN CIRCLE, SUITE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/911,569
FILING DATE: 23-Jul-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/039,780
FILING DATE: 16-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 23: US-09-911-569-23
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: SULLIVAN, SALLY A. REGISTRATION NUMBER: 32,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (303)499-808(
TELEFAX: (303)499-8089
INFORMATION FOR SEQ ID NO: 23:
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Gaps
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APPLICANT: LIU, Q1ang
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 289
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TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE. REFERENCE: 8325-0011.21 / S11-053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-990-186-289
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1larity 100.0%; Pred. No. 3.1e+05;
Conservative 0; Mismarches
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                                                         100.0%; Score 21; DB 10;
100.0%; Pred. No. 3.1e+05;
tive 0; Mismatches 0;
; OTHER INFORMATION: Peptide fragment of Thrombin US-09-909-122-3
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CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEGO ID NO 670
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 670, Application US/09990186 Publication No. US20030068675A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
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Publication No.
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TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
TITLE OF INVENTION: PEPTIDES
TITLE OF INVENTION: PEPTIDES
CURRENCE: 3033.1000-601
CURRENT APPLICATION NUMBER: US/09/904,090
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US 60/217,583
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Stimulation of Bone Growth With Thrombin
TITLE OF INVENTION: Peptide Derivatives
FILE REFERENCE: 3033.1002-001
                                                                                                                                                          Length 4;
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; OTHER INFORMATION: Polypeptide, fragment of thrombin US-09-904-090-1
                                                                                                                                                     Score 21; DB 10;
Pred. No. 3.1e+05;
); Mismatches 0;
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                                                                                            ; OTHER INFORMATION: Peptide fragment of Thrombin
US-09-909-348-3
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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Crowther, Roger S.
Simmons, David J.
Yang, Jinping
Redin, William R.
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ORGANISM: Artificial Sequence
                                       TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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SEQ ID NO 3
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TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 674. Application US/09990186
Publication No. US20030068675A1
GENERAL INFORMATION:
APPLICANT: LIU, QIANG
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT APPLICATION NUMBER: US/09/990,186
                                                                    FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-990-186-673
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                                                                                                                                                            Length 7;
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                                                                                                                                                        100.0%; Score 21; DB 9; I alarity 100.0%; Pred. No. 3.1e+05; Conservative 0; Mismatches 0;
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llarity 100.0%; Pred. No. 3.1e+05;
Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
                                                  ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 675
LENGTH: 7
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SOFTWARE: PatentIn Ver. 2
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Best Local Similarity
Matches 4; Conserva
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                             IYPE: PRT
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                                                                                    APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / 811-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DARE: 2001-11-20
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / 811-053
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
SOFTWARE: Patentin Vos: 4085
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / S11-US3
                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-990-186-671
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Pred. No. 3.1e+05;
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CURRENT FILLING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
                         Application US/09990186 o. US20030068675A1
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Publication No. US20030068675A1
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-09-990-186-671; Sequence 671, Ap; Publication No.
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US-09-990-186-673
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SOFTWARE: Pate
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RESULT 15
US-09-990-186-696
Sequence 696, Application US/09990186
Sequence 696, Application US/09990186
GENERAL INFORMATION:
APPLICANT: LIU, Olang
TITLE OF INVENTION: TRIPLETS BY 21NC FINGERS
TITLE OF INVENTION: TRIPLETS BY 21NC FINGERS
TITLE OF INVENTION: TRIPLETS BY 21NC FINGERS
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT PILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PATENTION OF GENERAL OF SEQUENCE: SEQUENCE: PATENTIAL OF SEQUENCE: SEQUENCE: SEQUENCE: CORRENT PATENTIAL OF SEQUENCE: PATENTE: PATEN
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Search completed: May 12, 2003, 15:59:09 Job time: 7.76 secs

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Gaps

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Query Match 100.0%; Score 21; DB 9; Length 7; Best Local Similarity 100.0%; Pred. No. 3.1e+05; Matches 4; Conservative 0; Mismatches 0; Indels

us-09-909-348-3.rpr

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GenCore version 5.1.4_p5_4578
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- protein search, using sw model OM protein May 12, 2003, 15:33:02; Search time 4.56 Seconds (without alignments) 84.328 Million cell updates/sec Run on:

US-09-909-348-3 21 Title: Perfect score:

1 RGDA 4 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	36K mlcrofibril-as	rsin - leech	ica		~	cal		_	trp RNA-binding pr	hypothetical prote	unknown protein en	ydaQ protein - Esc	cytochrome c551 -	conserved hypothet	cell surface glyco	hypothetical prote	Q,	hypothetical prote		hypothetical prote		ribosomal protein	hypothetical prote			μ	hypothetical prote	-	partial transposas
SUMMARIES	ឧ	A34467	A36453	G82812	S70093	S19623	E70535	AG3217	S62570	. I39905	B90870	G85748	E64884	268677	н82662	I68553	E82562	AH0620	E82696	G84240	D83771	A71054	C75089	E82962	S01566	T30673	E75273	F70976	B72538	F90230
	DB	7																•								7				
	Length	19	39	45	49	52	57	68	74	16	79	79	79	80	88	68	90	93	95	96	96	97	97	97	86	100	102	103	104	107
•	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21
	Result No.	-	7	m	4	ស	9	7	ω	6		11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	53

hypothetical prote hypothetical prote	conserved hypothet hypothetical prote	hypothetical prote ribosomal protein	ribosomal protein 50S ribosomal prot	phnQ protein - Esc hypothetical prote	30s ribosomal prot ribosomal protein	hypothetical prote 50s ribosomal prot	hypothetical prote hypothetical prote
T51207 E97566	AC2787 S14024	C82479 D71832	D64681 B81255	I35719 H75059	D84319 S62816	T03574 C86883	B72621 T37063
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108	110	115	116	121	124	124	126
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21	22	2 2	22	22	22	22	22
30 31	33	3.4	36 37	30 30 30 30	41 41	44 3	44
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ALIGNMENTS

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36K microfibril-associated protein - pig (fragment)
55K microfibril-associated protein - pig (fragment)
C; Species: Sus scrofa domestica (domestic pig)
C; Species: Sus scrofa domestica (domestic pig)
C; Species: Sus scrofa domestica (domestic pig)
R; Scossion: A34467
R; Kobayashi, R.; Tashima, Y.; Masuda, H.; Shozawa, T.; Numata, Y.; Miyauchi, K.; Haya
A; Title: Isolation and characterization of a new 36-kDa microfibril-associated glycop A; Reference number: A34467; MUID:90008913; PMID:2793866
A; Accession: A34467
A; Molecule type: protein
A; Residues: 1-19 < KOB>
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Best Local Similarity 100.

Matches 4; Conservative
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5 RGDA 8
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Gaps ö Query Match

100.0%; Score 21; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels

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1 RGDA 4 ò

1111 31 RGDA 34 g

RESULT 3 682812 hypothetical protein XF0386 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa

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100.0%; Score 21;
                                                                                                                                                                                                                                                                                                                        100.0%;
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Best Local Similarity 100.

Matches 4; Conservative
                                                                                                                           A;Accession: S19623
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-52 <MAZ>
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Best Local Similarity
Matches 4; Conserv
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A; Redolecule type: DNA
A; Residues: 1-45 < SIN>
A; Roblecule type: DNA
A; Residues: 1-45 < SIN>
A; Roblecule type: DNA
A; Residues: 1-45 < SIN>
A; Cross-references: GB:AE003890; GB:AE003849; NID:99105215; PIDN:AAF83196.1; GSPDB:GN001
A; Experimental source: Strain 9a5c
B; Simpson, A.J.G.; Rednach, F.C.; Arruda, P.; Abreu, F.A.; Acenclo, M.; Alvarenga, R.; Briones, M.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Briones, M.S.; Bueno, M.S.; Ferror, J. Briones, M.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueltra, M.L.; Remper, B.L.; Kitajima, J.P.; Krieger, J.E.; Krieger, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marcues, S.C.; Franco, M.V.; Martins, A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Fodriques, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Rodriques, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Reference number: A59328
A; Reference New A50428
A; Reference Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein (orf49) - Amycolatopsis methanolica
C;Species: Amycolatopsis methanolica
C;Date: 15-Feb-1997 $sequence_revision 13-Mar-1997 $text_change 07-May-1999`
C;Accession: 870093
R;Vrijbloed, J.W.; Jelinkova, M.; Hessels, G.I.; Dijkhuizen, L.
A;Vrijbloed, J.W.; Jalinkova, M.; Hessels, G.I.; Dijkhuizen, L.
A;Title: Identification of the minimal replicon of plasmid pMEA300 of the methylotrophid
A;Reference number: 870087; MUID:96154938; PMID:8596458
                        C; Accession: G82812
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Astronomys, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID: 20365717; PMID: 10910347
A; Note: for a complete list of authors see reference number A59328 below
A; Status: preliminary
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C;Species: Placobdella ornata
C;Species: Placobdella ornata
C;Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S19623
R;Mazur, P.; Henzel, W.J.; Seymour, J.L.; Lazarus, R.A.
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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A;Molecule type: DNA
A;Residues: 1-49 <VRI>A;Cross-references: EMBL:L36679
C;Genetics:
A;Start codon: GTG
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Best Local Similarity 100.
Matches 4; Conservative
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RGDA 26
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C;Species: Mycobacterium tuberculosis (Strain H3/KV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Uil-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: E70535
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamili, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987; PMID:9634230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:295972; GB:AL123456; NID:g3261790; PIDN:CAB09391.1; PID:e31919
A;Experimental source: strain H37Rv
C;Genetics:
Eur. J. Biochem. 202, 1073-1082, 1991
A;Title: Ornatins: potent glycoprotein IIb-IIIa antagonists and platelet aggregation
A;Reference number: S19566; MUID:92111479; PMID:1765068
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A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2577; PMID:11743193
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1.68 < CUR>
A; Cross-references: GB: AE008687; PIDN: AAL46157.1; PID:g17743927; GSPDB:GN00188
A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status; preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-57 <COL>
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                                                                                                                                                                                                                                                                                                                   Length 52;
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Pred. No. 1.6e+02;
0; Mismatches 0;
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Length 68;

DB 2;

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Species Bacherichia coll (Strain Crowned Crown
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: E64884
Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
Science 277, 1455-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64884
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                           protein ECs1930 [imported] - Escherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown protein encoded within prophage CP-933R [imported] - Escherichia coli (strain
                                                                                                                                                                                                                                                                                                              R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA, Res. 8, 11-22, 2001

A.; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A; Reference number: A99629; MUID:21156231; PMID:11258796

A; Status: preliminary
A; Status: preliminary
A; Residues: 1-79 <HAY>
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                     C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: B90870
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ilarity 100.0%; Pred. No. 2.4e+02;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.4e+02;
ive 0; Mismatches 0;
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Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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C; Species: Bacillus pumilus
C; Species: Bacillus pumilus
C; Species: Bacillus pumilus
C; Species: 13906
E; Accession: 13906
E; Accession: 13907
E; Hoffman, R.J.; Gollnick, P.
B; Hoffman, R.J.; Hoffman, P.
B; Hoffman, R. Hoff
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Experimental source: strain 972h-; cosmid c30D11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N'Alternate names: protein SPAC30D11.1
C'Species: Schlzosaccharomyces pombe
C'Date: 06-Dec-1996 #text_change 11-Jan-2000
C'Accession: S62370; 138587
R'Pearson, D.; Churcher, C.M.
submitted to the EMBL Data Library, November 1995
A; Reference number: S62559
                                                       Gapa
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                                                       Indels
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 4; Conservative 0; Mismatches 0;
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100.0%; Score 21; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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A;Map posttion: 1L
A;Introns: 1/3; 64/1.
C;Superfamily: rat ribosomal protein L38
C;Keywords: cytosol; protein blosynthesis; ribosome
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A; Residues: 1-74 <PEA>
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36 RGDA 39
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Length 88

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Score 21; DB 2;
Pred. No. 2.6e+02;
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Job time: 7.56 secs
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Best Local Similarity 100..
   A; Reference number: A59328
A; Contents: annotation
C; Genetics:
A; Gene: XF1562
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44 RGDA 47
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C; Superfamily: cytochrome c6; cytochrome c6 homology
C; Superfamily: cytochrome c6; cytochrome c6 homology
C; Superfamily: cytochrome c6; cytochrome c7; heme; iron; metalloprotein; oxidative phos
F; 1-77/Domain: cytochrome c6 homology <CYC>
F; 1-77/Domain: cytochrome c6 homology <CYC>
F; 10,13/Binding site: heme (Cys) (covalent) #status predicted
F; 14,59/Binding site: heme iron (His, Met) (axial ligands) #status predicted
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R; Samyn, B.; de Smet, L.; van Driessche, G.; Meyer, T.E.; Bartsch, R.G.; Cusanovich, M.P.
B.; de Schen, 236, 689-696, 1996
A; Title: A high-potential soluble cytochrome c-551 from the purple phototrophic bacteriu
A; Reference number: S68677; MUID: 96195682; PMID: 8612646
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A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:20365717; MID:10910347
A; Note: for a complete list of authors see reference number A59328 below
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A;Residues: 1-79 <BLAT>
A;Cross-references: GB:AE000232; GB:U00096; NID:g1787600; PIDN:AAC74428.1; PID:g1787608;
A;Experimental source: strain K-12, substrain MG1655
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Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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Pred. No. 2.4e+02;
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A; Residues: 1-88 <SIM>
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C;Accession: 168553
R;Horn, G.T.; Bugawan, T.L.; Long, C.M.; Manos, M.M.; Erlich, H.A.
Hum. Immunol. 21, 249-263, 1988
A;Tille: Sequence analysis of HLA class II genes from insulin-dependent diabetic indi
A;Reference number: 154290; MUID:88227495; PMID:3372263
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M35000; NID:9291960; PIDN:AAA35774.1; PID:9553265 C;Superfamily: class II histocompatibility antigen; immunoglobulin homology C;Reywords: 91ycoprotein
                                       C;Species: Homo sapiens (man)
C;Date: 04-Oct_1996 #sequence_revision 04-Oct-1996 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-89 <RES>
cell surface glycoprotein - human (fragment)
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pyrococcus
pyrococcus
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                                                                       May 12, 2003, 15:32:07; Search time 2.32 Seconds (without alignments) 71.511 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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RL6_HALMA
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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1 RGDA 4
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Q9cw73 m galactosy P72002 mycobacteri O08542 mus musculu P50619 bacillus su Q9h0t7 homo sapien Q9u1g2 lepidoglyph Q9bze7 homo sapien Q51659 paracoccus Q5kvc9 vibrio chol Q9hsb4 halobacteri Q9hn05 halobacteri P71687 mycobacteri			ite) Hirudinida; Hirudinea; lae; Macrobdella.	.T., Lazarus R.A.; gonist and platelet la decora.";	<pre>zarus R.A.; erved motif and distinct clotting.";</pre>	WITH PLATELET RECEPTORS . MAY PREVENT BLOOD FROM AGE OF INGESTED BLOOD. Y.	adhesion; 3D-structure. AFFINITY BINDIG DOMAIN (POTENTIAL). ATTACHMENT SITE. NG (IN N-3 ISOFORM). 5756FB70D36 CRC64;	Length 39; 0; Indels 0; Gaps		
	ស្	AA.	notation update) rican leech). Clitellata; Hiru es; Hirudinidae; 1	PubMed=2351655; it glycoprotein Ib-IIIa antagoni. tor from the leech Macrobdella di:10143-10147(1990).	, Laza conser	SCIENCE 204:1344'11940'(1954) FUNCTION: INHIBITS FIBRINGEN INTERACTION WITH EXPRESSED ON GLYCOPOTEIN IIB-IIIA COMPLEX. MAY CLOTTING DURING BITHER FEEDING AND/OR STORAGE C SIMILARITY: SOME, TO P.ORNATA ORNATINS.	Cell adhesion; 3D HIGH AFFINITY BIN CELL ATTACHMENT S MISSING (IN N-3 I: 3A3B35756FB70D36	В 1;		52 AA. date) update)
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202 203 204 221 222 224 224 224		STANDARD; 1. 15, Cr 1. 15, La		8; PubMed enzel W.J tent glyc ibitor fr 265:10143	ubMed G., GD pr rote1	EUNCE LOGGISSA-1594 (1994). FUNCTION: INHIBITS FIBRI EXPRESSED ON GLYCOPROPED CLOTTING DURING EITHER F SIMILARITY: HIGH, TO P.C SIMILARITY: SOME, TO THE	94. Platelet; 38 33 4384 MW;	Similarity 100 4; Conservative		STANDARD; 1. 22, Cr 1. 22, La 1. 38, La
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		ов 990 990	999 11a 12a 1411 10-6	902776; J.L., J n. A po lon in Chem.	3 BY 9427 .M.,	LARI	3.33 1901)	31mi 4;	A 4 A 34	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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       A MEDLINE-21840401; PubMed-11859360;

RA MEDLINE-21840401; PubMed-11859360;

RA WOOD V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Rood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Raber S., Brown D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Ra Gollins M., Connor R., Cronin N., Harris D., Hidayo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Holroyd S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,

RA Relton J., Simmond M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Marren T., Whitehead S.,

ROOdward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Taylor K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

R Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,

RA Lucas M., Rochet M., Galllardin C., Tallada V.A., Tanlede G.,
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                                                                                                                                                                                                                                               -i- FUNCTION: POTENT INHIBITOR OF FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. MAY PREVENT BLOOD FROM CLOTTING DURING EITHER FEEDING AND/OR STORAGE OF
                                                                                                                                                                                                                                                                                                                                          SIMILARITY: HIGH, TO THE OTHER P.ORNATA ORNATINS, AND TO M.DECORA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                  MEDLINE-92111479; PubMed-1765068; Mazur P., Henzel W.J., Seymour J.L., Lazarus R.A.; Ornatins: potent glycoprotein Inb-IIIa antagonists and platelet aggregation inhibitors from the leech Placobdella ornata."; Eur. J. Biochem. 202:1073-1082(1991).
Placobdella ornata (Turtle leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Rhynchobdellida; Glossiphoniidae; Placobdella.
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01-FEB-1996 (Rel. 33, Last sequence update)
15-TUN-2002 (Rel. 41, Last annotation update)
16-TUN-2002 (Rel. 41, Last annotation update)
16-TUN-2002 (Rel. 41, Last annotation update)
18-TUN-2002 (Rel. 41, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blood coagulation; Platelet; Cell adhesion.
SITE 42 44 CELL ATTACHMENT SITE.
SEQUENCE 52 AA; 5845 MW; BAS5CA740BEF4F09 CRC64;
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Pfam; PF02088; Ornatin; 1.
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Best Local Similarity
4; Conserve
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                                                                    NCBI_TaxID-6415;
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                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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-I- MISCELLANEOUS: There are two genes for L38 in S. Pombe.
-I- SIMILARITY: BELONGS TO THE L38E FAMILY OF RIBOSOMAL PROTEINS.
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription attenualion protein mtrB (Tryptophan RNA-binding attenuator protein) (Trp RNA-binding attenuation protein) (TRAP).
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NCBL_TaxID=1408;
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InterPro; IPR002675; Ribosomal_L38e.
Pfam; PF01781; Ribosomal_L38e; 1.
ProDom; PD010361; Ribosomal_L38e; 1.
Ribosomal protein; Multigene family.
SEQUENCE 74 AA; 8339 MW; C9006594DFCB11D3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus pumilus (Bacillus mesentericus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIKE STRUCTURE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L37879; AAA67544.1; -. HSSP; Q9X6J6; 1QAW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD:
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InterPro; IPR001147; Ribosomal_L21e. Pfam; PF01:157; Ribosomal_L21e; 1.
                                                                                                                                                                                                                                          EMBL; AJ248286; CAB50016.1; -.
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                                                                                                                                                                                                                                                                                                                                     100.08;
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                                                                                                                                                                                                                                                                                                           11378 MW;
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Best Local Similarity 100.
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                                         STRAIN-GE5 / Orsay;
Hellig R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           97 AA;
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69 RGDA 72
                                                                                                                                                                                                                                                                                                                                                                                       1 RGDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RL21_PYRHO
074001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus
                                                                                                                                                                                                                                                                                                           SEQUENCE
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    ð
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                                                                                                                                                                                                                                                                                                                                                                                STRAIN=D / ATCC 17899 / DSM 180;
MEDLINE-96195682; PubMed-8612646;
Samyn B., de Smet L., van Drieesche G., Meyer T.E., Bartsch R.G.,
Cusanovich M.A., van Beeumen J.J.;
"A high-potential soluble cytochrome c-551 from the purple
phototrophic bacterium Chromatium vinosum is homologous to cytochrome
c8 from denitrifying pseudomonads.";
Eur. J. Blochem. 235:689-696(1996).
-i- FUNCTION: MONOHEME CYTOCHROME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                      Chromatium vinosum.
Bacteria: Proteobacteria; gamma subdivision; Chromatiaceae;
Allochromatium.
                                                                            Score 21; DB 1; Length 76; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 21; DB 1; Length 80; 100.0%; Pred. No. 97;
                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COVALENT).
(HEME AXIAL LIGAND).
(HEME AXIAL LIGAND).
         Pfam; PF02081; TrpBP; 1.
PRINTS; PR00687; TRPRNAAP.
Transcripton regulation; RNA-binding.
SEQUENCE 76 AA; 8301 MW; 2218482351DA151D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EBD30A2815D07F93 CRC64;
                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cytochrome c-551 (C551).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEME (COVALENT).
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50s ribosomal protein Lile.
PPL/1B OR PAB0731.
                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR003088; Cyt_CI.
InterPro; IPR00234; Cyt_CID.
Pfam: PF00034; Cytochrome_c; I.
PRINTS; PR00606; CYTCHROMECID.
PROSITE; PS00190; CYTOCHROME_C; I.
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IRON
IRON
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                                                                           100.0%;
100.0%;
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 InterPro; IPR000824; TrpBP
                                                                                                        4; Conservative
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                                                                           Query Match
Best Local Similarity
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Matches 4; Conser
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                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1049;
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                                                                                                                                                        58 RGDA 61
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P80549;
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Q9UZP1;
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C551_CHRVI
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RL21_PYRAB
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                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Yamamoto S., Sekine M., Baba S. I., Kosuqi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.*I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii O73.";
'Pyrococcus abyss1 genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                  structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE L21E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEB. 3:33-70(1990).
SIMILARITY: BELONGS TO THE L21E FAMILY OF RIBOSOMAL PROTEINS.
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Pred. No. 1.2e+02;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6CEF3A2DB6A61E40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 39, Last sequence update) 50s ribosomal protein L21e. RPL21E OR PHS032.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribosomal protein; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01157; Ribosomal_L21e; 1.
PROSITE; PS01171; RIBOSOMAL_L21E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001147; Ribosomal_L21e.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                         Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.("Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";
                                                                 ö
                                                                                                                                                                                                                                                                                                                          "Human cytomegalovirus encodes a glycoprotein homologous to MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                          Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 98;
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                                                                Indels
                      6D5D229DBFBE0E51 CRC64;
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                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
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Pred. No. 1.2e+02;
Mismatches 0;
                                          Score 21; DB 1; Dred. No. 1.2e+02;
                                                                                                                                                                             01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Hypothetical protein UL19.
                                                                                                                                                              98 AA
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(Rel. 39, Last sequence update)
                                                                 Mismatches
                                                                                                                                                                                                                                        cytomegalovirus (strain AD169).
PROSITE; PS01171; RIBOSOMAL_L21E; 1. Ribosomal protein; Complete proteome SEQUENCE 97 AA; 11376 MW; 6D5D22
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EMBL; X17403; CAA35418.1; -.
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90269039; PubMed-2161319;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-88094735; PubMed-2827039;
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                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0;
                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                   class-I antigens.";
Nature 331:269-272(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                 Beck S., Barrell B.G.;
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PIR; S09782; S09782.
Hypothetical protein.
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     COMPLETE GENOME
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Q15772;
30-MAY-2000 (
30-MAY-2000 (
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95 RGDA 98
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69 RGDA 72
                                                                                   1 RGDA 4
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P16723;
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APG1_HUMAN
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                                                                                                                                                                                                                                                                                MEDLINE-96291890; PubMed-8663449;
Hsleh C.-M., Yoshizumi M., Endege W.O., Kho C.-J., Jain M.K.,
Kashiki S., de Los Santos R., Lee W.-S., Perrella M.A., Lee M.-E.;
"APEG-1, a novel gene preferentially expressed in aortic smooth muscle cella, is down-regulated by vascular injury.";
J. Biol. Chem. 271:17354-17359(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: NUCLEAR TANGED OF THE STREET OF THE MOST
                                                                                                                               Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eùteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GROWTH AND
                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Höminidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROMINENT FEATURES OF ARTIOSCLEROSIS.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - FUNCTION: MAY HAVE A ROLE IN REGULATING THE GROW DIFFERENTIATION OF ARTERIAL SMOOTH MUSCLE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
10-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2011 (Rel. 40, Last annotation update)
Aortic preferentially expressed protein 1 (APEG-1).
15-JUN-2002 (Rel. 41, Last annotation update)
Aortic preferentially expressed protein 1 (APEG-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 AA.
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HSSP; P56276; lTLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U57099; AAC50599.1;
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                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                        NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
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062407;
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HSSP; P56276; 1TLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGDA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trust T.J.;
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                                                                                                   MEDLINE-96221890; PubMed-8663449;
Hsieh C.-M., Yoshizumi M., Endege W.O., Kho C.-J., Jain M.K.,
Rashiki S., de Los Santos R., Lee W.-S., Perrella M.A., Lee M.-E.;
Rashiki S., de Los Santos R., Lee W.-S., Perrella M.A., Lee M.-E.;
cells, is down-regulated by vascular injury.";
J. Biol. Chem. 271:17354-17359(1996).
I- FUNCTION: MAY HAVE A ROLE IN REGULATING THE GROWTH AND
DIFFERENTIATION OF ARTERIAL SWOOTH WUSCLE CELLS.
-- SUBCELLULAR LOCATION: Nuclear.
-- TESUE SPECIFICITY: PREPERENTIALLY EXPRESSED IN DIFFERENTIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN DIFFERENTIATED ARTERIAL SMOOTH MUSCLE CELLS (ASMC) IN THE MEDIAL LAYER OF THE AORTA.
Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 21; DB 1; Length 113; 100.0%; Pred. No. 1.4e+02; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, P562/0; JILL.
MGD; MGI:109282; Appell.
MGD; MGI:109282; Appell.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003598; Ig_C2.
SMART; SM00407; Ig.; 1.
SMART; SM00408; IGC2; I.
Immunoglobulin domain; Nuclear protein.
DOMAIN
34 95 IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                 ARTERIAL SMOOTH MUSCLE CELLS (ASMC).
-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAX-2000 (Rel. 39, Created)
30-MAX-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aortic preferentially expressed protein 1 (APEG-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 AA.
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                  SEQUENCE FROM N.A.
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RGDA 88
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MEDLINE-99120557; PubMed-9923682;
Alm R.A. Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Healtoobacter pylori.";
Nature 397:176-180(1999).
-I- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50S ribosomal protein Li7.
RPLQ OR JHP1212.
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria: Proteobacteria: epsilon subdivision; Helicobacter group;
WEAKLY DETECTED IN BRAIN AND TESTIS AND TO A LESSER EXTENT IN ORGANS RICH IN STRIATED MUSCLE OR VISCERAL SMOOTH MUSCLE. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 113 AA; 12668 MW; B213C366A759A363 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EBC77780E2F2F3A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 21; DB 1; I 100.0%; Pred. No. 1.4e+02;
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; 14; 1.
SMART; SMO0408; IGc2; 1.
Immunoglobulin domain; Nuclear protein.
34 95 IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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InterPro; IPR000456; Ribosomal_L17.
Pfam; PF01196; Ribosomal_L17; 1.
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TIGRFAMS; TIGR00059; L17; 1.
PROSITE; PS01167; RIBOSOMAL_L17; 1.
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SEQUENCE 116 AA; 13392 MW;
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Best Local Similarity
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(Rel. 35, Last sequence update) (Rel. 40, Last annotation update)
                               50S ribosomal protein L17.
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                                                RPLQ OR MPN192 OR MP639.
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                                                             Mycoplasma pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=64091;
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                                                                                                                                                                                                                                                                                                                                                                     pneumoniae.
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09HPE9:
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                                                                                                                                                                                                                                                                                                                                                                                                                     Tomb J.-F., White O., Kerlauge A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weldman J.M., Fujil C., Bowman C., Watthey L., Wallin E., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                 Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pylori.";
Nature 388:539-547(1997).
-1- SIMILARITY: BELONGS TO THE L17P FAWILY OF RIBOSOMAL PROTEINS.
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              Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 1; Length 116; Pred. No. 1.4e+02;
           Score 21; DB 1; Length 11
Pred. No. 1.4e+02;
Mismatches 0; Indels
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                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                      116 AA
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                                            0; Mismatches
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Pfam; PF01196; Ribosomal_L17; 1.
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TIGREAMS; TIGR00059; L17; 1.
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RL17_MYCPN STANDARD; E
LO SE17_MYCPN STANDARD; E
C OS9547;
DT 01-NOV-1997 (Rel. 35, Created)
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           Query Match

Best Local Similarity 100.0%;

Matches 4; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-26695 / ATCC 700392;
                                                                                                                                                                                                                                                                50S ribosomal protein L17. RPLQ OR HP1292.
                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-210;
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                                                                                                        104 RGDA 107
                                                                            1 RGDA 4
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P56042;
                                                                                                                                                      RESULT 13
RL17_HELPY
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                               SEQUENCE FROM N.A.
STRAIN-AFCC 29342 / M129;
STRAIN-AFCC 29342 / M129;
HIDDET H., Himmelreich R., Plagens H., Herrmann R.;
"Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma promomoniae comprising the dnaA region, the atp operon and a cluster of ribosomal protein genes.";
Nucleic Acids Res. 24:628-639(1996).
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-1- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
NCBI_raxID=2104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-AVCC 29342 / M129;
MEDLINE-97105885; Pubmed-8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
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Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3A627DB7EBF8C62E CRC64;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
RPSBE OR VNG1668G.
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SEQUENCE 124 AA; 14245 MW; 3A6271
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InterPro; IPR000456; Ribosomal_L17.
Pfam; PF01196; Ribosomal_L17; 1.
TIGREAMS; TIGR00059; L17; 1.
PROSITE; PS01167; RIBOSOMAL_L17; 1.
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Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; "Genome sequence of Halobacterium species NRC-1."; "Genome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGRO0307; S8e; 1.
PROSITE; PS01193; RIBOSOWAL_S8E; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 124 AA; 13515 MW; B7038CF79A83742B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         5; IPR001047; Ribosomal_S8E.
F01201; Ribosomal_S8e; 1.
PD005658; Ribosomal_S8E; 1.
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Pfam; PF01201
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Search completed: May 12, 2003, 15:36:39 Job time : 3.32 secs

1 RGDA 4 ||||| 47 RGDA 50

07 05 Q882d8 oryza sativ Q827w3 salmonella Q96x9x xylella fas Q98xe9x rhizobium 1 Q9xe8x bacillus ha Q9hxa8 pseudomonas Q9hxa8 bacteroides Q98x39 molluscum c Q98x29 pseudomonas Q9xxn9 deinococcus Q9xrn9 deinococcus

Q9HTA8 Q8RM68 Q98239

Q9HR67

Q827W3 Q9PDS1 Q98FE9 Q9KE84

10 16 17 17 16

006257 mycobacter1 Q50073 mycobacter1 Q9ybk7 aeropyrum p

Q29783 homo saplen Q9pau0 xylella fas Q9dk41 human 1mmun Q9fzt5 pseudomonas Q9nm57 leishmanla

Q8w3b8 oryza sativ. Q9pd18 xylella fas Q8zv78 pyrobaculum Q95y01 caenorhabdi Q29783 homo saplen

Q9PD18 Q82V78

Q8TK40

Q9PAU0 Q9DK41

5 16 15

29171 sus scrofa Q92ki0 rhizobium m

Q8x8q7 escherichia Q8tk40 methanosarc

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A SIMPSON A.J.G., Relnach F.C., Arrada P., Abreu F.A., Acencio M., Rabluller-Musol, T., Arrada D.E., Bala G.S., Baptista C.S., RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S., RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Bueno M.R.P., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., R. Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Farinca S.C., Franco M.C., Frohme M., Furlan L.R., R. Facincani A.P., Ferreitra A.J.S., Ferreitra V.C.A., Ferro J.A., R. Farinca J.S., Rranca S.C., Franco M.C., Frohme M., Fullan L.R., R. Ho P.L., Hoheisel J.D., Junqueira M.L., Remper E.L., Kitajima J.P., R. Achos E.G.M., Langes C.R., Machado J.A., Marchas E.B., Lalgret F., Lambais M.R., Leite L.C.C., R. Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marinc C.L., Martins E.A., Martins E.M.F., Martins C.L., Martins E.M.F., Matcho C.L., Martins E.M.F., Matcho C.L., Martins E.M., Nacimento A.L.T., Nonteiro-vitorello C.B., Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Moon D.H., Nobrega F.G., Minnes L.R., Diveira M.A., Paris A., Marcha B.R., Rodrigher D.A., Paris A., Drevicta M.A., Perduca G.A.G., Pereitra H.A. Jr., Pesquero J.B., Roberto P.G., Rodrigher V., de Rosa A.J.M., Ge Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Xf0386.
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MEDLINE-20365717; PubMed-10910347;
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NCBI_TaxID=2371;
8888
Q9PGB6
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Q9PGB6
O9pgb6 xylella fas O9xdv3 erythrobact QBrh3 thermoanaer QBruzl zea mays (m O9n041 macaca fasc QBrud5 zea mays (m O6773 mycobacteri QBqsB3 chimpanzee QBLS7 thizoblum 1 QBsyq0 ralstonia s QBnyk agrobacteri QBvyk agrobacteri Spyt28 ralstonia s
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                                                                            May 12, 2003, 15:32:37 ; Search time 9.04 Seconds (without alignments) 91.171 Million cell updates/sec
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          GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                        protein search, using sw model
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Q8RUZ1
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Q8RUD5
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006773
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"A complete sequence of T. ter
Genome Res. 12:689-700(2002).
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EMBL; AF498485;
EMBL; AF498486;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBI_TaxID-119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *Nucleotide sequences of genes coding for photosynthetic reaction
centers and light-harvesting proteins of Erythrobacter litoralis and
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da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C.; "The genome sequence of the plant pathogen Xylella fastidiosa."; "The genome sequence of the plant pathogen Xylella fastidiosa."; "The GOO3890; AAP83196.1; -BMBL; AE003890; AAP83196.1; -Hypothetical protein; Complete proteome.
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Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                                                                     h Similarity 100.0%; Score 21; DB 16; Length 45; Similarity 100.0%; Pred. No. 2.9e+02; 4; Conservative 0; Mismatches 0; Indels
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB027515; BAA78669.1;
Interpro; PS0007352; Acyl-CoA_dh.
PROSITE; PS00073; ACYL-COA_DH_2; UNKNOWN_1.
SEQUENCE 48 AA; 4980 MW; D663EAD05EA8079B CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein TrE2436.
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01-NOV-1999 (TrEMBLrel. 12; Last sequence update)
01-DEC-2001 (TrEMBLrel. 19; Last annotation update)
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Pred. No. 3.1e+02;
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MEDLINE=21992816; PubMed=11997336;
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Similarity 100.0%;
4; Conservative 0
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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NCBI_TaxID=94771;
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27 RGDA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09XDV3;
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Q8R7H3
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Q9XDV3
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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Suzuki Y., Sugano S., Hashimoto K.;
                                                                                                                                                                                          Gaps
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Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
Morgante M., Rafalski J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            frequency, haplotype structure and linkage disequilibrium in a maize inbred lines.";
ltted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Unnamed protein product.
Unamed protein product.

Budacae fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukarybta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin; Cercopithecidae;
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                                                                                                                                       Length 54;
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                                     EMBL, AE013185, AAM25571.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 54 AA; 6252 MW; 0A9C818C07DD905B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 AA; 5959 MW; 5C09DAC7224451D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acetyl-CoA C-acyltransferase-like protein (Fragment)
tengcongensis genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
                                                                                                                                     100.0%; Score 21; DB 16; 100.0%; Pred. No. 3.5e+02;
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100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
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NON_TER 1 1
SEQUENCE 55 AA; 5959 MW;
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                                                                                                              Local Similarity
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SEQUENCE FROM N.A.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. IVAND, CV. D71-4HT, AND CV. H60;
Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
Morgante M., Rafalski J.A.;
"SNP frequency, haplotype structure and linkage disequilibrium in
ellite maize inbred lines.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ., Garnier T., Churcher C., Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Deviln K., Feltwell T., Gentles S., Hamin N., Holroyd Hernsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Ollver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., Deciphering the blology of Mycobacterium tuberculosis from the Nature 393:537-544 (1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF498474; AAM14490.1; -.
EMBL; AF498476; AAM14492.1; -.
EMBL; AF498479; AAM14495.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Acetyl-CoA C-acyltransferase-like protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 AA; 6185 MW; DC4596C76E4451A8 CRC64;
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Last annotation update)
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100.0%; Pred. No. 3.7e+02;
iive 0; Mismatches 0;
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100.0%; Score 21; DB 16;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acyltransferase; Transferase.
NON_TER 1 1
SEQUENCE 57 AA; 6185 MW; I
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01-MAR-2002 (TEMBLEE). 20,
Hypothetical protein Rv0666.
RV0666 OR MTC1376.10C.
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                     NCBI_TaxID=4577;
                                                                                                                                             Zea mays (Maize)
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01-JUL-1997
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006773
                ACCOCCOS DETAILS OF THE SECOND OF THE SECOND
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-VARIOUS STRAINS;
Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "SNP frequency, haplotype structure and linkage disequilibrium in elite maize inbred lines.";
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"Isolation of full-length cDNA clones from macaque brain cDNA libraries.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB046091; BAB01673.1; -.
SEQUENCE 57 AA; 6250 MW; 300DE0464A4897A9 CRC64;
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                                                                                                                                                                      Length 57;
                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 21, Last annotation update)
Acetyl-CoA C-acyltransferase-like protein (Fragment).
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                                                                                                                                                                 100.0%; Score 21; DB 6; I 100.0%; Pred. No. 3.7e+02;
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                                                                                                                                                                                                                       Mismatches
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"SNP frequency, haplotype st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF498487; AAM14503.1
                                                                                                                                                                                                                  4; Conservative
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Best Local Similarity
'-had 4; Conserve
                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
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33 RGDA 36
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SEQUENCE
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Q8RUD4
ID Q8RUD4
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RESULT 9 Q8QS83

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LM28.210.
Leisbhmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                      Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat W., Biottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Signier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
                                                                                                                                                                   Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 21; DB 16; Length 64; 100.0%; Pred. No. 4.1e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; Complete proteome.
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                                                01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein RSc1708.
RSC1708 OR RS02894.
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(TrEMBLrel. 21, Last sequence update)
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         PRT;
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                                                                                                                                                                                                                                                                                                                                     MEDLINE-21681879; PubMed-11823852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL646066; CAD15410.1; -.
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       PRELIMINARY;
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01-OCT-2000 (TrEMBLrel.
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Best Local Similarity

4, Conserve
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                        NCBI_TaxID-305;
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QBUJK6
ID QBUJK6;
AC QBUJK6;
DT 01-UUN-2002 (
DT 01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
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                                                                                                                                                                                                                    Ralstonia.
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SEQUENCE
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Q9N7K3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                          Davison A.J., Akter P., Dolan A., Wright K.M., Addison C., Alcendor D.J., Hayward G.S., McGeoch D.J.;
"The human cytomegalovirus genome revisited.";
Submitted (FEB-2002) to the EWBL/GenBank/DDBJ databases.
EMBL; AF480884.1; -.
SEQUENCE 58 AA; 6789 MW; 27400659BBD2BAD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 21; DB 16; Length 5
100.0%; Pred. No. 3.8e+02;
ive 0; Mismatches 0; Indels
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SEQUENCE 59 AA; 6059 MW; 4EE77EF3940E6633 CRC64;
                                                                                                                                                                                                                                                         chimpanzee cytomegalovirus.
Vituses; dsDNA vituses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID-188763;
                                                                                                                                                                                       Last sequence update)
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                     58 AA
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                                                                                                                                                                 Created)
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EMBL; AP002996; BAB48386.1; -.
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01-MAR-2002 (TrEMBLrel. 20, L
Hypothetical protein ms10897.
                                                                                                                                                            -JUN-2002 (TrEMBLrel. 21, -JUN-2002 (TrEMBLrel. 21, -JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
nes 4; Conservative
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Best Local Similarity 100.
Matches 4: Conservative
                                                                                                                     PRELIMINARY;
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24 RGDA 27
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2 RGDA 5
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RESULT 10 Q98LS7

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Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H., Lo C.F., Rou G.H.;
Indertification of a nucleocapsid protein (VP35) gene of shrimp white spot syndrome virus and characterization of the motif important for targeting VP35 to the nuclei of transfected insect cells.";
                                                                              Tsal M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J., Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
"Identification and characterization of a shrimp white spot syndrome virus (WSOW) gene that encodes a novel chimeric polypeptide of cellular type thymidine kinase and thymidylate kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databa:
EMBL, AF332093; AAL33202.1; -
EMBL; AF40570; AAL89202.1; -
SEQUENCE 70 AA; 7417 MW; 6C31737FF210FB62 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
101-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypotheital protein RSc3433.
RSC3433 OR RS01813.
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100.0%; Pred. No. 4.5e+02;
11ve 0; Mismatches 0;
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100.0%; Pred. No. 4.5e+02;
tive 0; Mismatches 0;
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                                                         MEDLINE-20517548; PubMed-11062040;
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Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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RGDA 19
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Q8XTW3
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"The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Hountel K., Gordon J., Yaudin M., Tartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Clelo C., Slater S.;
Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens CS8.
                                                                                                                                                                                              MEDLINE-21608550; PubMed-11743193; MeDLINE-21608550; PubMed-11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L., Chen I., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chilland P., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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MEDLINE-21548311; PubMed-11689662;
Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
"Complete genome sequence of the shrimp white spot bacilliform
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SEQUENCE FROM N.A.
Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 protein; Plasmid; Complete proteome.
68 AA; 8005 MW; 5CABE406D75F93A8 CRC64;
                                                                    Agrobacterium tumefaciens (strain C58 / Arcc 33970)
01-JUN-2002 (TrEMBLE). 21, Last annotation update)
Hypothetical protein Atu5470.
ATU5470 OR AGR_PAT_693.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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EMBL; AE007916; AAK90845.1; -.
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NCBI_TaxID-92652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 294:2323-2328(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
Les 4; Conservative
                                                                                                                                     Rhizobiaceae; Rhizobium.
NCBI_TaxID-176299;
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RGDA 39
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SEQUENCE 68
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08VAV0; Q8VAV0

virus.

Best Loca Matches

36

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RESULT 14 Q8VAV0 us-09-909-348-3.rspt

Search completed: May 12, 2003, 15:38:43 Job time : 12:04 secs

Scoring table:

Total number

Searched:

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Database

Perfect score:

Title:

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Platelet membrane
Thrombin peptide d
Bovine zeta 2 pret
Bovine prethrombin
Bovine prothrombin
Thrombin B chain a
Modified RGD pepti
                                                                                                                                                                                                        Human CD4/thrombin
Human CD4-thrombin
Prothrombin (PT).
Human prothrombin
Human prothrombin
                                                             Mutant thrombin R2
Mutant thrombin R2
Mutant thrombin R3
Mutant thrombin W5
Mutant thrombin W5
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Mutant thrombin W5
                                                                                                                                                       Human mature throm
Amino acid sequenc
Human prethrombin
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Human preprothromb
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thrombin
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                                      Mutant
Mutant
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Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Material for medical treatment comprises new peptide - used covering injuries, promoting adhesion of bio-tissues, bone reinforcing and nerve regeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell growth/adhesion promoting peptide #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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AAB83282
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AAW11546
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                                                                                                                                              AR<sub>7</sub>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97JP-0140885
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JP10316581-A.
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 AAW83414;
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  Human zeta 2 preth
Human thrombin Asn
Wild-type thrombin
Mutant thrombin K5
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Human thrombin pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                     May 12, 2003, 15:31:22; Search time 71.5 Seconds (without alignments) 46.591 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                  / SIDS2/gcdata/geneseq/geneseqp-embl/AA1980.DAT:*
/ SIDS2/gcdata/geneseq/geneseqp-embl/AA1981.DAT:*
/ SIDS2/gcdata/geneseq-embl/AA1981.DAT:*
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/SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:*
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                                                                                                                                                                                                                                                         908470
             GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                       of hits satisfying chosen parameters:
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141
1 AGTRYKPDEGKRGDACEGDSGGPFV 25
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                                                               OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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AAE22563
AAE20159
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AAW11545
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AAR74776
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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5 YRPDEGKRGDACEGDSGGPFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a new nerve regenerative material which contains a peptide immobilised to a base which consists of a polysaccharide gel such as alginic acid. Sequences AAB12886-B12899 represent examples of the peptides used in the nerve regeneration material. The peptide containing material causes nerve cell prolliferation and also causes axonal extension. The material can be used for the treatment of central or peripheral nervous system disorders,
The present invention describes a material for medical treatment which comprises one or more peptides of the formula XADEGJIMProQY, or their salts, immobilised on a substrate: where X = H, CH3CO or CH3COLys;
A = Ser or Thr: D = ILe, Val or Leu; E = Lys or Arg; G = ILe, Val or Leu; J = Gly or Ala; L = ILe, Val or Leu; M = Gly or Ala; Q = Gly, Ala or Gly-Lys-Lys-Gly; Y = OH or NH2. Also described is an agent for cell growth promotion and/or cell adhesion promotion containing the above peptide or its salt as the active component. The peptide and its salt can be used for covering injuries, promoting adhesion of blotissues, bone reinforcing and nerve regeneration. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nerve regeneration; nerve cell proliferation; axon extension; treatment;
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l nervous system disorder; peripheral nervous system disorder;
disorder; head injury; cerebrovascular disorder.
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                                                                                                                                                                                                                                specifically claimed peptide of the present invention
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llarity 100.0%; Pred. No. 1.6e-07;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                       Score 121; DB 20;
Pred. No. 1.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nerve tissue regenerative peptide SEQ ID #8
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                                                                                                                                                                                                                                                                                                    85.8%; Scc.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TANI/) TANIHARA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-415772/36
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Best Local Similarity
Matches 21; Conserv
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Best Local Similarity
Matches 21; Conserv
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neutrophil cell chemotactic agent. (1) has vulnerary and antiinflammatory activities. (1) is useful as a potent neutrophil cell chemotactic agent and for generating antibodies against the peptides, which are useful for modulating neutrophil recruitment to a wound site for enhancing or inhibiting inflammation and early effects of wound healing. Neutrophil response to (1) is specific, since monocytes and fibroblasts do not show any expression of the receptor to which (1) binds. The present sequence represents a human thrombin receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain peptide which is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New synthetic neutrophil cell chemotactic peptides, useful for generating antibodies for modulating neutrophil chemotaxis in immune response and wound healing -
                                                                                                                                                                                                                                                                                                                                            Neutrophil cell chemotactic; wound healing; inflammation; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; proteolytically activated receptor for thrombin; neutrophil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a synthetic peptide (I) which is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                        Human thrombin receptor binding domain peptide SEQ ID NO:8.
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Pred. No. 1.6e-07;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHRY-) CHRYSALIS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Column 6; 15pp; English.
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                                                                                                                                             AAB70363 standard; peptide; 23 AA.
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ramakrishnan S;
                                                                                                                                                                                                                                          02-MAY-2001 (first entry)
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Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6184342-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-OCT-1994;
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Gaps

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Indels

28-OCT-1994;

Carney DH,

Homo sapiens

14-MAR-2002

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Stimulating growth and repair of cartilage, useful for treating e.g. arthritis, by local administration of an agonist of non-proteolytically activated thrombin receptor
                                                                                                                                                                                                                                                                The invention relates to a method of stimulating growth and repair of cartilage. The method involves administering to the site, an agonist of non-proteclytically activated thrombin receptor (NPAR). The method is used in human or veterinary medicine for the treatment of arthritic
                                                                                                                                                                                                                                                                                                                                             joints and damage/loss of cartilage caused by traumatic injury. Also chouforcytes may be cultured in presence of NPAR agonist to provide cells for implantation at sites requiring growth/repair of cartilage. The present sequence is human thrombin peptide derivative which serves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombin; revascularisation; vascular occlusion; tissue repair; vulnerary; vasotropic; cardiant; anglogenesis; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombin-derived peptide used to promote cardiac tissue repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12..23
/note= "serine esterase conserved sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "thrombin receptor binding domain" 12..23
                                                                  Stiernberg J, Bergmann J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.8%; Score 121; DB 23;
100.0%; Pred. No. 1.6e-07;
11ve 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM50858 standard; Peptide; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.5°,
100.0%; Pre
0;
                                                                                                                                                                                                                             Claim 12; Page 25; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 YKPDEGKRGDACEGDSGGPFV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JUL-2001; 2001WO-US21944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-2000; 2000US-217583P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 YRPDEGKRGDACEGDSGGPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                         (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 85.8
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TEXA ) UNIV TEXAS SYSTEM
                                                                  Carney DH, Crowther RS,
                                                                                                      WPI; 2002-268953/31
                                                                                                                                                                                                                                                                                                                                                                                                                                 a NPAR agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vulnerary; vasc
therapy; human,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200204008-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carney DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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AAM50858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to novel synthetic peptides and antibodies which are potent chemotactic agents for neutrophils. The peptides of the invention minic the activity and role of the cleavage fragment of the proteolytically activated receptor for thrombin (PART). They are useful for generating or modulating neutrophil cell chemotactic migration or are useful for modulating neutrophil recultment to a wound site for an antibody. In particular, the peptides of the invention enhancing or inhibiting inflammation and early effects in wound healing. They are also useful for modulated neutrophil chemotaxis in immune response. The present sequence is high affinity receptor binding domain of human thrombin. This peptide is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cartilage repair, arthritic joint, traumatic injury, ly activated thrombin receptor; NPAR; chondrocyte;
                                                                                                                                                                                                                                                                                                                                                                            New synthetic peptide neutrophil cell chemotactic agents, useful for stimulating or modulating neutrophil cell chemotactic migration, particularly for modulating neutrophil recruitment during immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
chemotactic agent; PART; inflammation; wound healing; chemotaxis; immune response; vulnerary; thrombin; receptor binding domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.8%; Score 121; DB 23;
100.0%; Pred. No. 1.6e-07;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; implantation; thrombin peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human thrombin peptide derivative #2.
                                                                                                                                                                                                                                                            (CHRY-) CHRYSALIS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE20159 standard; peptide; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 3; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 YKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                           response or in wound healing
                                                                                                                                                                             05-FEB-2001; 2001US-0777328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 YKPDEGKRGDACEGDSGGPFV
                                                                                                                                                                                                                                                                                                   Ramakrishnan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-2002 (first entry)
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Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                         WPI; 2002-371207/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cartilage growth; canon-proteolytically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AA;
                                                                                             JS2002032314-A1
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Sequence

Promoting cardiac tissue repair, stimulating revascularisation, stimulating vascular endothelial cell proliferation, and inhibiting vascular occlusion by using angiogenic thrombin derivative peptide

WPI; 2002-179665/23.

19-JUL-2001; 2001WO-US22668.

31-JAN-2002

Homo sapiens

AAE20159;

RESULT 5 AAE20159

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20-JUL-2000; 2000US-219800P

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Indels

Length 23;

cleavage of prothrombin (PTh) to thrombin (Th) by prothrombinase (I), at a site remote from the catalytic site of (I) comprises: (a) preparing a solution containing 0.05-20 mu M substrate (S), that includes a protease cleavage site and exosite-binding determinant; 0.05-200 nm factor vs; 30-500 micro M phospholipids (PL); test inhibitor (A) in buffer of pH 7-9, containing 1-10 nm calcium ions but no calcium-chelating agent; (b) initiating catalytic cleavage of (S) by adding an aliquot of factor Xa (to final concentration 0.05-200 nm) so that there is an excess of va over Xa, forming a S/(I) complex; (c) withdrawing aliquots of the The present peptide comprises a thrombin-derived peptide, TP508, that includes a thrombin receptor binding domain sequence (see also AAM50856) and a serine esterase conserved sequence (see also eardiectissue repetide is used in a claimed method for promoting cardiac tissue repair. It is administered during or following cardiac surgery by injection into cardiac tissue, and may be formulated as a sustained release formulation. The thrombin derivative peptide is also used in claimed methods of stimulating revascularisation, stimulating vascular endothelial cell An exosite assay has been developed for inhibition of the catalytic Exosite assay for agents that inhibit catalytic cleavage of prothrombin - at sites away from the active site of prothrombinase, also new inhibitors, potentially useful as anticoagulants proliferation, inhibiting vascular occlusion, and inhibiting restenosis following balloon angloplasty, in which case it may be coated onto the catheter. Prothrombin; exosite assay; anticoagulant; blood clot; thrombin; cardlovascular disease; stroke; haematological disorder. 85.8%; Score 121; DB 23; Length 23; 100.0%; Pred. No. 1.6e-07; .ive 0; Mismatches 0; Indels Disclosure; Page 44-45; 61pp; English. AAW99115 standard; protein; 116 AA Claim 4; Page 19; 24pp; English 25 3 YRPDEGKRGDACEGDSGGPFV 23 98WO-US10840. 98US-0081030 97US-0048864 5 YKPDEGKRGDACEGDSGGPFV Human zeta 2 prethrombin 2. (first entry) Best Local Similarity 100. Matches 21; Conservative WPI; 1999-070237/06. (UYEM-) UNIV EMORY 23 AA; Krishnaswamy S; Homo sapiens WO9855130-A1 14-MAY-1999 28-MAY-1998; 08-APR-1998; 06-JUN-1997; 10-DEC-1998 Sequence Query Match AAW99115; RESULT 7 셤 ä

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Gaps

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reaction mixture, quenching them; and (d) assaying for concentration of Th. Alternatively, in the initial solution S is replaced by the same concentration of Xa (less than the amount of Va), and reaction is started by adding S. Also described in the present invention are inhibitors (A') had having 1650 less than 1 mu M identified by this assay. (A') are potentially useful as a new class of anticoagulants for treatment of cardiovascular disease, stroke and haematological disorders. The method substrate specificity in catalytic formation of Th. The present sequence represents human zeta 2 prethrombin 2. Prothrombin mutants having one or more changes in amino acid sequence compared with the natural protein and having 0-10% (preferably 0-0.25% of the activity of the natural protein are claimed, provided that the changes in amino acid sequence do not affect the capacity of the mutants to bind to specific ligands and receptors. The mutants have greatly reduced clotting activity and are useful as antagonists of thrombin inhibitors such as hirudin, heparin and anti-thrombin III. The mutations may also result in changes to the in vivo half-life Gaps Prothrombin; mutant; mutein; platelet aggregation; blood clotting; coagulation; reduce; decrease; hirudin; heparin; anti-thrombin III; antagonist; D99N. /note= "Wild-type Asp residue has been replaced Prothrombin mutants with reduced clotting activity - useful as antagonists of thrombin inhibitors or for anticoagulant therapy ö Length 116; Indels Schlokat 85.8%; Score 121; DB 20; illarity 100.0%; Pred. No. 6.9e-07; Conservative 0; Mismatches 0; Eibl J, Falkner F, Fischer B, Mitterer A, /label- thrombin_Asn99 Misc-difference 99 Location/Qualifiers AAW11545 standard; Protein; 259 AA. Example 3; Page -; 73pp; German. 25 47 YRPDEGKRGDACEGDSGGPFV 67 Human thrombin Asn99 mutant. 96WO-AT00105 5 YKPDEGKRGDACEGDSGGPFV (first entry) WPI; 1997-065455/06 Local Similarity hes 21; Conserv (IMMO) IMMUNO AG. Homo sapiens 12-JUN-1996; 13-JUN-1995; WO9641868-A2 01-0CT-1997 27-DEC-1996. Synthetic AAW11545; Seguence Query Match Protein Best_Loca] Matches AAW11545 RESULT 888888888888 ð g

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prothrombin. The half-life may be reduced to less than 10 minutes the mutant prothrombin may have an extended half-life of more than
                                                                                                                                                                                                                               Gaps
                     1 hour, making it useful as an anticoagulant and to inhibit side-
effects of anti-coagulant treatment. They are converted to inactive
thrombin and are able to compete with native, active thrombin for
blinding to receptors. The present sequence represents the thrombin
mutant which is derived by trypsin cleavage of a specifically
claimed human prothrombin mutant in which Asp at position 419 is
changed to Asn. The thrombin Asn99 mutant was found to have only
0.24% of the activity of wild-type thrombin on a chromogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombin derivs with segregated pro- and anticoagulant activities useful for treating thrombotic disorders but also diagnosis,
                                                                                                                               (Note: This sequence does not appear in the specification and has been produced by modifying the wild-type sequence of human prothrombin which appears in figure 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence reresents wild-type (reference) thrombin. Mutants of this sequence (AAR7476-80 and AAR76033-41) have at least 80% homoology with thrombin, and are capable of protein-c activation without significant fibrinogen clotting activity, and vice versa (specifically have a ratio of protein-C activity to fibrinogen clotting activity to fibrinogen clotting activity of less than 0.5 or greater than 2 compared to
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombin; oligonucleotide-directed mutagenesis; procoagulant;
                                                                                                                                                                                                    85.8%; Score 121; DB 18; Length 259; 100.0%; Pred. No. 1.4e-06; 1.ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                               anticoagulant; protein engineering; ss.
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                                                                                                                                                                                                                                                                                                                                      AAR74775 standard; Protein; 295 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsiang M;
                                                                                                                                                                                                                                                                 190 YRPDEGKRGDACEGDSGGPFV 210
                                                                                                                                                                                                                                                   5 YKPDEGKRGDACEGDSGGPFV 25
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93US-0152657
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                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of tumours, etc.
                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           Wild-type thrombin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-NOV-1994;
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12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9513385-A.
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                                                                                                                                                                                                                                                                                                                                                            AAR74775;
                                                                                                                                                                                Sequence
                                                                                                                                                                                                      Query Match
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Gaps
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    recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombin derivs with segregated pro- and anticoagulant activities useful for treating thrombotic disorders but also diagnosis,
thrombin). The mutant thrombin sequences, produced in recombinan' each culture or by in vitro methods, and are used to treat thrombotic conditions, particularly during cardiac bypass surgery and in cases of septic shock.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombin; oligonucleotide-directed mutagenesis; procoagulant;
                                                                                                                                                           Length 295;
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                                                                                                                                                         Score 121; DB 16;
Pred. No. 1.6e-06;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anticoagulant; protein engineering; ss
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                                                                                                                                        85.8%; Scc.
100.0%; Pre
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                                                                                                                                                                                                                                                                        226 YKPDEGKRGDACEGDSGGPFV 246
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                                                                                                                                                                                                                                                5 YKPDEGKRGDACEGDSGGPFV 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant thrombin K52A, R233A.
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93US-0152657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37..295
/note= "n
                                                                                                                                                                                                      21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leung LLK,
                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                              295 AA;
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12-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR74776;
                                                                                                                 Sequence
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AAR74777

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Protein

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The mutant thrombin sequence, generated by oligonucleotide-directed mutagenesis, has at least 80% homology with thrombin, and is capable of protein-c activation without significant fibrinogen clotting activity, and vice versa (specifically, it has a ratio of protein-C activity to fibrinogen clotting activity of less than 0.5 or greater than 2 compared to thrombin). The mutant thrombin is produced in recombinant cell culture or by in vitro methods, and is used to treat thrombotic conditions, particularly during cardiac bypass surgery and in cases of septic shock.
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useful for treating thrombotic disorders but also diagnosis,
treatment of tumours, etc.
                                                                                                                                                                    mutagenesis; procoagulant;
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Pred. No. 1.6e-06;
0; Mismatches 0;
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37..295
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/note= "mature protein"
                                                                                                                                                                                      protein engineering; ss
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  AAR74778 standard; Protein; 295 AA.
                                                                                                                                                                  Thrombin; oligonucleotide-directed anticoagulant; protein engineering;
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100.0%; Pre
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93US-0152657,
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                                                                                   (first entry)
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les 21; Conservative
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12-NOV-1993;
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llarity 100.0%; Pred. No. 1.6e-06;
Conservative 0; Mismatches 0;
Pred. No. 1.6e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Glu in wild-type" 37..295
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Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
                                                                                   226 YKPDEGKRGDACEGDSGGPFV 246
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93US-0152657
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Best Local Similarity
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12-NOV-1993;
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Gaps

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Sequence

RESULT 12 AAR74778

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Length 295; Indels Thrombin; oligonucleotide-directed mutagenesis; procoagulant; anticoagulant; protein engineering; ss.

Protein

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The mutant thrombin sequence, generated by oligonucleotide-directed mutagenesis, has at least 80% homology with thrombin, and is capable of protein-C activation without significant fibrinogen clotting activity, and vice versa (specifically, it has a ratio of protein-C activity to fibrinogen clotting activity of less than 0.5 or greater than 2 compared to thrombin). The mutant thrombin is produced in recombinant cell culture or by in vitro methods, and is used to treat thrombotic conditions, particularly during cardiac bypass surgery and in cases of septic shock.
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100.0%; Pred. No. 1.6e-06;
ive 0; Mismatches 0;
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Matches 21; Conservative
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                                                 /note= "Glu in wild-type" 37..295
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/note= "mature protein"
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/note= "mature protein"
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12-NOV-1993;
Homo sapiens
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Protein

RESULT 14 AAR74780

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Gaps

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The mutant thrombin sequence, generated by oligonucleotide-directed mutagenesis, has at least 80% homology with thrombin, and is capable of protein-C activation without significant fibrinogen clotting activity, and vice versa (specifically, it has a ratio of protein-C activity to fibrinogen clotting activity of less than 0.5 or greater than 2 compared to thrombin. The mutant thrombin is produced in recombinant cell culture or by in vitro methods, and is used to treat thrombotic conditions, particularly during cardiac bypass surgery and in cases of septic shock.
                                                                                                                                                        Thrombin derivs with segregated pro- and anticoagulant activities useful for treating thrombotic disorders but also diagnosis, treatment of tumours, etc.
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Gibbs CS, Leung LLK, Tslang M;
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Query Match 85.8%; Score 121; DB 16; Length 295; Best Local Similarity 100.0%; Pred. No. 1.6e-06; Matches 21; Conservative 0; Mismatches 0; Indels (5 YKPDEGKRGDACEGDSGGPFV 25 a õ

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0; Gaps

Search completed: May 12, 2003, 15:36:06 Job time : 72.5 secs

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Gaps
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Sequence 2
Sequence 4
Patent No.
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Patent No. 6146824
GENERA INFORMATION:
APPLICANT: BAR-SHAVIT, RACHEL
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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100.0%; Pred. No. 5.3e-11;
ive 0; Mismatches 0;
                                        US-08-955-471-1
US-09-667-570A-3
PCT-US92-10242-1
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APPLICATION NUMBER: US/08/981,088
FILING DATE: 27-JAN-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: OLIFF, JAMES A
REGISTATION NUMBER: 27,075
REFERENCE/DOCKET NUMBER: JAO 40455
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                           5270178-16
                                                                                                                              5270178-14
                                                                                                                                             5270178-15
                                                                                                                                                                                         5270178-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 YKPDEGKRGDACEGDSGGPFV 25
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS: LENGTH: 23 amino acids
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Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-981-088-2
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Sequence 2, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
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Appli
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                                                                                             // Search time 24 Seconds
(without alignments)
30.649 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3,
Sequence 4,
Sequence 51,
Patent No. 52
Patent No. 52
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Sequence 2,
Sequence 2,
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Patent No.
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                              /ogn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
            GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-330-594-8

US-08-344-483-52

US-08-38-269-10

US-09-410-882-10

US-09-295-411-4

US-08-955-471-4

US-08-955-471-4

US-09-117-708-14

US-09-908-972A-3

US-08-463-953-3

US-08-463-953-3

US-08-952-967-8

US-08-952-967-8

US-08-952-967-8

US-08-952-967-8

US-08-952-967-8

US-08-981-088-3

US-08-981-088-3

US-08-981-088-3

US-08-981-088-4

US-08-944-483-51
                                                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
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US-09-065-872-2
US-09-667-570A-2
                                                                                                                                                                                                                                                                 262574 seqs, 29422922 residues
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Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                  May 12, 2003, 15:33:37
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                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 2000000000
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141
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Match 1
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08338368
Patent No. 6110721
GENERAL INFORMATION:
APPLICANT: GIBBS, CRAIG S.
APPLICANT: TSIANG, MANUEL
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND COAGULATION
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,368
FILING DATE: 14-NOV-1994
                                                                                                                                                                                                                                  85.8%; Score 121; DB 4; ]
100.0%; Pred. No. 7.2e-10;
11ve 0; M1smatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 121; DB 3;
Pred. No. 8.2e-10;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,038
FILING DATE: 10-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: GILEAD SCIENCES, INC
353 LAKESIDE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.00,
100.0%; Prv
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELECOMMUNICATION INFORMATION: TELEPHONE: 415-574-3000
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                                                                                                                                                       TOPOLOGY: 'linear'
; MOLECULE TYPE: No. 6232456e
US-08-944-483-52
                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 259 amino acida TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                         single
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MOLECULE TYPE: protein

US-08-338-368-2
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                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 21; Conserva
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CALIFORNIA
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Best Local Similarity
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                                                                                                                                   STRANDEDNESS:
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                                                                                        GENERAL INFORMATION:
APPLICANT: CAREY. DARRELL H.
APPLICANT: CAREY. SHYAM
TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS
FILE REFERENCE: CHBP:002
CURRENT APPLICATION NUMBER: US/08/330,594C
CURRENT APPLICATION DATE: 1994-10-28
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PALENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide
US-08-330-594-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 23
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85.8%; Score 121; DB 4;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 21; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BECKET, Cheryl L. REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF THE PROSTATE
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NOVEL SERINE BAND METHODS US
                                                    Sequence 8, Application US/08330594C
Patent No. 6184342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 52, Application US/08944483
Patent No. 6232456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Abbott Laboratories
100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COHEN, MAURICE
COLLITES, TRACET I.
FRIEDMAN, PAULA N.
GRANADOS, EDWARD N.
KLASS, MICHAEL R.
RUSSELL, JOHN C.
STEWART, KENT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 YKPDEGKRGDACEGDSGGPFV
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: STROUPE, STER
TITLE OF INVENTION: NOVI
TITLE OF INVENTION: AND
TITLE OF INVENTION: OF NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                      US-08-330-594-8
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                                                                                                                                                                                                                                                                      SEQ ID NO 8
LENGTH: 23
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STATE:
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Protease-Derived Polypeptides and eptide Antibodies; Systems and Therapeutic Methods
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STREET: 10666 No. 5679639th Torrey Pines Road, TPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBBR: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUBBR: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 121; DB 4;
Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-Peptide Antibodies, Sifor Inhibiting Coagulation 10
                                                                                                                                                                                                               NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CRI-001CP2
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARCTERIFICS:
LENGTH: 376 amino acids
                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/558,269
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: US 07/847,800
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSR1263.0C1
                        US/09/410,882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: GTIffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine Proteas
TITLE OF INVENTION: Anti-Peptide P
TITLE OF INVENTION: for Inhibiting
NUMBER OF SEQUENCES: 10
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Best Local Similarity 100.
Matches 21; Conservative
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: Ilnear
; MOLECULE TYPE: protein
US-09-410-882-10
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US-09-410-882-10
Sequence 10, Application US/09410882
Sequence 10, Application US/09410882
GENERAL NO. 6287561
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 26
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                          Sequence 10, Application US/08558269
Patent No. 5961973
GENERAL INFORMATION:
APPLICANT: Crea, Roberto
TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 85.8%; Score 121; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,269
FILING DATE: 13-NOV-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,800
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: GRI-001CP2
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 YRPDEGRRGDACEGDSGGPFV 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 227-7400
TELERAX: (617) 227-5941
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 YKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-558-269-10
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                   STREET: 60 St
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02109
                                                                                                                                                                                                                                                                                                                      COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: M. COUNTRY:
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INFORMATION FOR SEQ ID NO:

Gaps

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Length 579;
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APPLICANT: BOLLSCHWEILER, Claus; SCHWIDT, Martin;
APPLICANT: HOEFFERN, HAIS WOLFgang; SCHWEDEN, Juergen;
APPLICANT: and RUEBSAMEN, Klaus
TITLE OF INVENTION: Thrombin muteins as antidote for
TITLE OF INVENTION: thrombin inhibitors
                            NAME/KET: Region
LOCATION: 1..320
OTHER INFORMATION: /note= "Prothrombin Light Chain"
                                                                                                                                                                                                                /note= "Prothrombin Heavy Chain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM AT-compatible, Pentium processor OPERAITMS SYSTEM; Windows 95
SOFTWARE: WordPerfect version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,708
FILING DATE: O4-ANG-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                          Score 121; DB 2;
Pred. No. 1.7e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.7e-09;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09117708 Patent No. 6060300 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match

Best Local Similarity 100.0%; P

Matches 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   510 YKPDEGKRGDACEGDSGGPFV 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 579 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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                                                                                                                                                HAME/KEY: Region
CCATION: 321..579
CTHER INFORMATION:
US-08-955-471-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20036
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US92-10242-4
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                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
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Anti-Peptide Antibodies, Systems and Therapeutic Methods
for Inhibiting Coagulation
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                                                                                                                                                                                                                   NAME/KEY: Region
LOCATION: 1..320
OTHER INFORMATION: /note= "Prothrombin Light Chain"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC
                                                                                                                                                                                                                                                                                                                                                                                                                             /note- "Prothrombin Heavy Chain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
JURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

85.8%; Score 121; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSRI263.0C1
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FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FILLING, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI;
TELECOMMUNICATION:
FILESCOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08955471
Patent No. 5968751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510 YKPDEGKRGDACEGDSGGPFV 530
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                         i: 579 amino acida
amino acid
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amino acid
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOLECULE TYPE: protein HYPOTHEICAL: NO
                                                                                TOPOLOGY: 11near
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Griffin, J
APPLICANT: MESTERS, R
TITLE OF INVENTION: S
TITLE OF INVENTION: A
                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: Region
; LOCATION: 321..579
; OTHER INFORMATION:
US-08-295-411-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 La Jolla
: CA
                                                                                                                                             HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                         LENGTH:
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Length 615;
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APPLICANT: Holly, Richard D.
APPLICANT: FOSter, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,972A
FILING DATE: 19921230
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentieth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 121; DB 1;
Pred. No. 1.8e-09;
0; Mismatches 0;
                                                                                                                                                                                           FILING DATE: 19921230
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S 07/860,701
FILING DATE: 31-MRR-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDBR: 0S 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PARMELES, Steven W
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-12-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
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ZIP: 94105
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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             COUNTRY:
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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    Serine Protease-Derived Polypeptides and
Anti-Peptide Antibodies, Systems and Therapeutic Methods
for Inhibiting Coagulation
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100.0%; Pred. No. 1.7e-09;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-998-972A-3

Sequence 3, Application US/07998972A

Fatent No. 54/6777

FORDERAL INFORMATION:

APPLICANT: Foster, Donald C.

TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSES: Townsend and Townsend

STREET: One Market Plaza, Stewart Street Tower,

STREET: Twentieth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Region
LOCATION: 321..579
CHER INFORMATION: /note= "Prothrombin Heavy Chain"
PCT-US92-10242-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "Prothrombin Light Chain
                                                                                                       ADDRESSEE: Office of Patent Counsel, The Scripps ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
AUFLICATION DATA:
FILLING DATE: 19921118
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18 NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: 34,163
TELEPHONE: 619-554-2937
TELEPHONE: 619-554-2937
TELEPHONE: 619-554-2937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 579 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 21; Conservative
TITLE OF INVENTION: Seri
TITLE OF INVENTION: Anti
TITLE OF INVENTION: for
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Twentieth FI
CITY: San Francisco
STATE: CA
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LOCATION: 1.320
OTHER INFORMATION:
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85.8%; Scilarity 100.0%; P. Conservative 0;
                                                                                          5 YKPDEGKRGDACEGDSGGPFV 25
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MEDIUM TYPE: Floppy disk
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TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein PCT-US92-11357-3
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Best Local Similarity
Matches 21; Conserva
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OPERATING SYSTEM:
    Query Match
Best Local Similarity
Matches 21; Conserva
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COUNTRY: US
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PCT-US92-11357-3
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MEDIUM TYPE: Floppy disk
COMPUTER: IND PC compatible
SOUTHWER IND PATE: BLOOS/MS-DOS
SOUTHWER: PPELICATION DATA:
APPLICATION NUMBER: US/08/462,261
FILING DATE: 05-JUN-1995
CLASSIFICATION NUMBER: US 07/998,972
FILING DATE: 31-MR-1992
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-DEC-1991
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: PAINCHEASTON NUMBER: 31,990
REFERENCE/COKET NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3. Application US/08462261
Patent No. 5527692
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...ukussee: __ cuuness:
STREET: One Market Plaza, Stewart Street Tower,
STREET: Twentleth Floor
CITY: San Francisco
STATE: CA
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                                  REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 1395;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9603
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 anino acids
TYPE: amino acid
TYPE: amino acid
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SEQUENCE CHRARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W
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Length 615;
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APPLICANT: HOLLY, Richard D.
APPLICANT: FOSter, Donald C.
TILLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: Townsend and Townsend
STREET: Twentieth Floar
STREET: Twentieth Floar
CITY: San Francisco
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CURRENT APPLICATION DATA:
APPLICATION UNMER: PCT/US92/11357
FILING DATE: 19921230
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Pred. No. 1.8e-09;
Score 121; DB 1; Pred. No. 1.8e-09;
                                            Mismatches
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APPLICATION WUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION:
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SYSTEM: PC-DOS/MS-DOS
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Schlokat, Uwe
Mitterer, Artur
Falkner, Falko-Guenter
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REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 1395
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
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; Patent No. 6086871
                                                                                                          546 YKPDEGKRGDACEGDSGGPFV 566
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APPLICANT:
APPLICANT:
APPLICANT:
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Query Match 85.8%; Score 121; DB 3; Length 622; Best Local Similarity 100.0%; Pred. No. 1.8e-09; Matches 21; Conservative 0; Mismatches 0; Indels
APPLICANT: Eibl, Johann
TITLE OF INVENTION: PROTHROMBIN DERIVATIVES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Larder
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,967
FILING DATE: 26-JAN-1998
CLASSIFICATION NUMBER: US/08/952,967
FILING DATE: 12-JUN-1996
PRIOR APPLICATION NUMBER: AT A 1006/95
FILING DATE: 13-JUN-1995
FILING DATE: 13-JUN-1995
FILING DATE: 13-JUN-1995
ATPONENTY-AGERT INFORMATION:
AAPPLICATION NUMBER: AT A 1006/95
FILING DATE: 13-JUN-1995
ATPONENTY-AGERT INFORMATION:
AAPPLICATION NUMBER: AT A 1006/95
FILING DATE: 13-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: ISACSON, JOHN P.
RECISTRATION NUMBER: 33,715
REFERENCE/FOCKET NUMBER: 065691/0127
TELECOMONICATION INFORMATION:
TELEFENNE: (202)672-5309
TELEFAX: (202)672-5399
TELEFAX: (202)672-5399
TELEK: 904.36
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
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// MOLECULE TYPE: protein
US-08-952-967-8
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0; Gaps

Search completed: May 12, 2003, 15:40:40 Job time: 24 secs

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Bublication No. US20020182205A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CIOWTHER, ROGER S.
APPLICANT: SIMMONS, David J.
APPLICANT: SIMMONS, David J.
APPLICANT: Redin, William R.
ITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROWBIN
ITLE OF INVENTION: STIMULATION OF BONE COURTENT PEPTIDE DERIVATIVES
FILE REFERENCE: 3033.1002-004
CURRENY ETLING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/909,122
CURRENY ETLING DATE: 2001-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 25
TWORE: DATE
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Best Local Similarity 100.0%; Pred. No. 8.5e-13;
Matches 25; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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US-09-909-348-5
Sequence 5, Application US/09909348
; Patent No. US20020042373A1
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ORGANISM: Artificial Sequence

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Sequence 6, Appli
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                                                                                                                                                                                             May 12, 2003, 15:38:52 ; Search time 48.5 Seconds (without alignments) 47.436 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO7_NEW_DUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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                         GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-909-348-5

US-00-909-122-5

US-10-050-611-4

US-10-050-688-5

US-10-050-688-6

US-09-777-328-8

US-09-904-090-3

US-09-904-090-3

US-09-904-998-837A-45

US-09-998-837A-41
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US-10-182-263-3
US-10-182-263-4
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141
1 AGTRIKPDEGKRGDACEGDSGGPFV 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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                                                                                                                                          OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Gaps

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TITLE OF INVENTION: METHODS OF THERAPY WITH THROWBIN DERIVED
TITLE OF INVENTION: PEPTIDES
TITLE OF INVENTION: PEPTIDES
CURRENT APPLICATION NUMBER: US/10/050,611
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 09/904,090
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2000-07-12
TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED TITLE OF INVENTION: PEPTIDES FILE REFERENCE: 3033.1000-000 CURRENT APPLICATION NUMBER: US/10/050,611 CURRENT FILING DATE: 2002-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.8%; Score 121; DB 9; 1 100.0%; Pred. No. 4.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.2e-10;
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100.0%; Pred. No. 4.2e-10
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOTHER INFORMATION: valine is amidated as CONH2 US-10-050-611-4
                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:

; OTHER INFORMATION: human fragment of thrombin
US-10-050-611-3
                                                                                                          PRIOR APPLICATION NUMBER: 09/904,090
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
ENGTH: 23
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SOTTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LEMOTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10050611 Publication No. US20020187933A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10050688 Publication No. US20020198154A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 YKPDEGKRGDACEGDSGGPFV 23
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Best Local Similarity
Matches 21; Conservē
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LOCATION: 23
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                                                APPLICANT: Crowther, Roger S.
APPLICANT: Stiernberg, Janet
APPLICANT: Stiernberg, Janet
APPLICANT: Stiernberg, Janet
APPLICANT: Bergmann, John
TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re
TITLE REPERENCE: 3033.1003-001
CURRENT APPLICATION NUMBER: US/09/909,348
PRIOR APPLICATION NUMBER: US 60/219,800
PRIOR PILING DATE: 2000-07-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 141; DB 10; Best Local Similarity 100.0%; Pred. No. 8.5e-13; Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Peptide fragment of Thrombin US-09-909-348-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: Peptide fragment of Thrombin US-09-909-122-5
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FILE REFERENCE: 3033.1002-001
GURRENT APPLICATION NUMBER: US/09/909,122
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/219,300
                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 25
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APPLICANT: Redin, William R.
TITLE OF INVENTION: Stimulation Of Bone (
TITLE OF INVENTION: Peptide Derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGTRYRPDEGKRGDACEGDSGGPFV 25
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Publication No. US20020187933A1
                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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Crowther, Roger S
Simmons, David J.
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APPLICANT: Carney, Darrell H.
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LENGTH: 25
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Patent No. US20020032314A1

Patent No. US20020032314A1

APPLICANT: CAREY, DARRELL H.

APPLICANT: RAMAKRISHNAN, SHYAM

TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS

TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS

CURRENT APPLICATION NUMBER: US/09/777,328

CURRENT FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 08/330,594

PRIOR FILING DATE: 1994-10-28
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US-09-777-328-8
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TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
TITLE OF INVENTION: PEPTIDES
FILE REPERENCE: 3033.1000-001
CURRENT APPLICATION NUMBER: US/09/904,090
CURRENT FILING DATE: 2001-07-12
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US-09-904-090-3
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Pred. No. 4.2e-10;
0: Mismatches 0;
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Pred. No. 4.2e-10;
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PRIOR FILLING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 4
SORTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.8%; Scu.
100.0%; Pre
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                                                  Application US/09777328
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Best Local Similarity 100.0%; P.
Matches 21; Conservative 0;
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity
Matches 21; Conserva
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SEQ ID NO 8
LENGTH: 23
                           -09-777-328-8
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                                  TITLE OF INVENTION: STIMULATION OF CARFILAGE GROWTH WITH
TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
TITLE OF INVENTION: RECEPTOR
FILE REPERBUCE: 3033.1003-004
CURRENT APPLICATION NUMBER: US/10/050,688
CURRENT FILING DATE: 2002-01-16
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,800
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 23;
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APPLICANT: Crowther, Roger S.
APPLICANT: Stlernberg, Janet
APPLICANT: STRUMULATION OF CARTILAGE GROWTH WIT
TITLE OF INVENTION: RECEPTOR
TITLE OF INVENTION: RECEPTOR
FILE REFERENCE: 3033.1003-004
CURRENT APPLICATION NUMBER: US/10/050,688
CURRENT APPLICATION NUMBER: US/10/050,688
CURRENT APPLICATION NUMBER: 002-01-16
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FRASESO for Windows Version 4.0
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Pred. No. 4.2e-10
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: peptide fragment of thrombin US-10-050-688-5
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Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
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Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
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ORGANISM: Artificial Sequence
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Stiernberg, Janet
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; OTHER INFORMATION: CONH2
US-10-050-688-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     SEQ ID NO 5
LENGTH: 23
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NPPLICANT: MACDOUGAII, JOHN R
TILLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
TILLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                            Gaps
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Pred. No. 4.1e-08;
); Mismatches 1
                                                                                                                                                                                             Score 114; DB 9;
Pred. No. 4.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: U.S.S.N. 60/215,906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
RIOR FILING DATE: 1999-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-04-07
APPLICATION NUMBER: U.S.S.N. 60/197,080
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APPLICATION NUMBER: U.S.S.N. 60/232,677
FILING DATE: 2000-09-15
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APPLICATION NUMBER: U.S.S.N. 60/195,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: U.S.S.N. 60/181,347 FILING DATE: 2000-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: U.S.S.N. 60/194,195
FILING DATE: 2000-04-03
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                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 41, Application US/09898837A
Publication No. US20030077697A1
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Taupier Jr., Raymond
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Gerlach, Valerie L
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                                                                                                                                                                                             80.9%;
95.2%;
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Burgess, Catherine
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95.2%;
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PRIOR FILING DATE: 2000-11-1
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 45
LENGTH: 250
                                                                                                                                                                                           Query Match
Best Local Similarity 95.2
Matches 20; Conservative
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Vernet, Corine
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Best Local Similarity 95.2
Matches 20; Conservative
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                                                                                                      TYPE: PRT
CORGANISM: Bos taurus
US-09-898-837A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Bos taurus
US-09-898-837A-41
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TLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
TLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: c-terminal amidated fragment of human thrombin
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                                 TITLE OF INVENTION: STIMULATION OF BONE GROWTH WITH THROMBIN
TITLE OF INVENTION: PEPTIDE DERIVATIVES
FILE REFERENCE: 303.1002-004
CURRENT APPLICATION NUMBER: US/10/050,692
CURRENT FILING DATE: 2002-01-16
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
SPRIOR FILING DATE: 2000-07-19
SEQ ID NO 6
SEQ ID NO 6
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Pred. No. 1.1e-09;
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LOCATION: (23)...(23)

COTHER INFORMATION: valine is amidated as CONH2
US-10-050-692-6
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PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
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APPLICATION NUMBER: U.S.N. 60/195,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: U.S.S.N. 60/197,080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGT--KPDEGKRGDACEGDSGGPFV 23
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nupier Jr., Raymond
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Irgess, Catherine
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                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity 92.0%;
Matches 23; Conservative
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PRIOR APPLICATION NUM
PRIOR APPLICATION NUM
PRIOR, FILING DATE: 20
PRIOR, PELLING DATE: 20
PRIOR PAPLICATION NUM
PRIOR FILING DATE: 20
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US-09-898-837A-45
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DB 9; Length 419;
APPLICANT: Grincell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/189199
PRIOR PILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 419
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                                                                                                                                                                                                                                                                                                                                 Score 71;
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Job time : 49.5 secs
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                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-10-182-263-4
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Best Local Similarity
Matches 13; Conserv
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Pred. No. 0.05;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 71; DB Pred. No. 0.05
                                                                                    APPLICANT: Gerlitz, Bruce E
APPLICANT: Gerlitz, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVEWTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARRE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3. Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Grimell, Brian W
TILE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-07-11
PRIOR FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
                                 Sequence 1, Application US/10182263 Publication No. US20030022354A1 GENERAL INFORMATION:
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Best Local Similarity 81.2%;
Matches 13; Conservative
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Best Local Similarity 81.2
Matches 13; Conservative
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US-10-182-263-3
                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: HOI
US-10-182-263-1
                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1
LENGTH: 419
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LENGTH: 419
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US-10-182-263-4
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Gaps

3; Indels

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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 protein search, using sw model OM protein May 12, 2003, 15:33:02 ; Search time 28.5 Seconds Run on:

(without alignments) 84.328 Million cell updates/sec

US-09-909-348-5 141 1 AGTRYRPDEGKRGDACEGDSGGPFV 25 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched: Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
-	121	85.8			TBHO	thrombin (EC 3.4.2
7	117	83.0	236	~	C42696	thrombin (EC 3.4.2
e	114	80.9	625	Н	TBBO	
4	108	76.6		7	F42696	thrombin (EC 3.4.2
S	103	73.0	235	~	D42696	thrombin (EC 3.4.2
9	103	73.0	235	~	E42696	thrombin (EC 3.4.2
7	100	70.9	236	7	142696	thrombin (EC 3.4.2
æ	66	70.2	239	~	G42696	thrombin (EC 3.4.2
6	92	65.2	617	7	S10511	_
10	92	65.2		7	A35827	thrombin (EC 3.4.2
11	79	56.0	235	7	H42696	thrombin (EC 3.4.2
12	71	50.4	461	Н	KXHU	t
13	70.5	50.0		7	832794	trypsin-like prote
14	67	47.5	225	~	S45356	probable serine pr
15	29	47.5	417	Н	S00845	hepsin (EC 3.4.21.
16	67	47.5	1524	~	T30337	polyprotein - Afri
17	65	46.1	275	7	S40007	trypsin (EC 3.4.21
18	65	46.1	482	-	EXRT	
19	64.5	45.7	191	~	148158	
20	64	45.4	191	7	S54115	complement factor
21	64	45.4	246	7	DBHU .	complement factor
22	64	45.4	309	~	B49878	coagulation factor
23	. 64	45.4	456	-	KXBO	protein C (activat
24	64	45.4	1004	~	T30338	oviductin (EC 3.4.
25	64	45.4	2616	~	A57096	nudel protein prec
26	63	44.7	161	~	162744	coagulation factor
27	63	44.7	461	-	JX0210	protein C (activat
58	63	44.7	488	Н	EXHO	coagulation factor
59	62	44.0	263	-	155608	complement factor

tryptase (EC 3.4.2	protein C (activat	coagulation factor	plasmin (EC 3.4.21	tissue kallikrein	probable serine pr	limulus clotting e	t-plasminogen acti	coagulation factor	serine proteinase	coagulation factor	coagulation factor	plasma kallikrein	trypsin (EC 3.4.21	serine proteinase	trypsin-like prote	
JC4171	\$18994	EXCH	PLBO	A37938	T35195	A23689	UKHUT	184621	A30100	JQ0419	EXBO	KOHUP	TRCY1	555493	865465	
7	Н	Н	Н	7	7	-	Ч	~	Н	ď	٦	-	П	~	~	
274	461	475	812	260	285	375	562	282	392	459	492	638	237	250	254.	
44.0	44.0	44.0	44.0	43.6	43.3	43.3	43.3	42.9	42.9	42.9	42.9	42.9	42.6	42.6	42.6	
62	62	62	62	61.5	61	19	61	60.5	60.5	60.5	60.5	60.5	09	9	9	
30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45	
						:.										

ALIGNMENTS

thrombin (EC 3.4.21.5) precursor [validated] - human N;Alternate names: coagulation factor II N;Contains: prothrombin

C; Species: Homo sapiens (man)
C; Date: 30-Nov-1980 #sequence_revision 22-Jul-1994 #text_change 08-Dec-2000
C; Date: 30-Nov-1980 #sequence_revision 22-Jul-1994 #text_change 08-Dec-2000
C; Accession: A29351; A00914; B00914; A37549; A37550; I51952
R; Degen, S.J.F.; Dayle, E.W.
B; Degen, S.J.F.; Dayle, E.W.
A; Title: Nucleotide sequence of the gene for human prothrombin.
A; Reference number: A29351; MUID:88077877; PMID:2825773

A; Accession: A29351

A; Molecule type: DNA

A; Residues: 1-622 < CDEG>
A; Cross-references: GB:M17262; GB:M33691; NID:g558069; PIDN:AAC63054.1; PID:g339641
R; Degen. S.J.F.; Macdillivray, R.T.A.; Davie, E.W.
R; Degen. S.J.F.; Macdillivray, R.T.A.; Davie, E.W.
A; Degen. S.J.F.; Macdillivray of the complementary deoxyribonucleic acid and gene coding A; Reference number: A00914; MUID:83231469; PMID:6305407

A;Molecule type: mRNA A;Residues: 8-163,'N',165-622 <DE2> A;Cross-references: GB:V00595; GB:J00307; NID:g37128; PIDN:CAA23842.1; PID:g1335344

A; Accession: A00914

A; Accession: B00914
A; Molecule type: DNA
A; Residues: 188-11 < DE3>
R; Walz, D.A.; Hewett-Emmett, D.; Seegers, W.H.
Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
A; Reference number: A37549; MUID:77193964; PMID:266717

A; Accession: A37549
A; Molecule type: protein
A; Readduces: 44-118, M', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'MV', 196-3
A; Readduces: 44-118, M', 120, 'S', 122-163, 'I', 165-175, 'A', 177-182, 'T', 184-193, 'MV', 196-3
B; Butkowski, R.J.; Elilon, J; Downing, M.R.; Mann, R.G.
J; Biol. Chem. 252, 4942-4957, 1977
A; Title: Primary structure of human prethrombin 2 and alpha-thrombin.
A; Reference number: A37550; MUID: 77207112; PMID: 873923

A; Molecule type: protein A; Residues: 315-334, N',336-348, NV,350-368, NV,370-397, NV,399-413, NV,415-484, NV,4 B; Rabiet, M.J.: Blashill, A.; Furie, B.; Furie, B.C. J. Biol. Chem. 261, 13216-13215, 1986 A; Reference number: A37551; MUID:87008532; PMID:3759958

A; Contents: annotation; activation cleavages R; MacGillivray, R.T.; Irwin, D.M.; Guinto, E.R.; Stone, J.C. Ann. N. T. Acad. Sci. 485, 73-79, 1986 A; Title: Recombinant genetic approaches to functional mapping of thrombin. A; Reference number: 151952; MUID: 87182874; PMID: 3471151

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-2,'RI',5-100 <RES>

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Rybark, C. H.; Tullnaky, A. Biochemistry 25, 3977-3982, 1986
Biochemistry 25, 3977-3982, 1986
A;Title: Three-dimensional structure of the kringle sequence: structure of prothrombi A;Title: Three-dimensional structure of the kringle sequence: structure of prothrombi A;Reference number: A3755; MID: 86296631; PMID: 3741841
A;Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms K;Irwin, D.M.; Ahern, K.G.; Pearson, G.D.; MacGillivray, R.T.A.
Biochemistry 24, 6854-6861, 1985
A;Title: Characterization of the bovine prothrombin gene.
A;Reference number: A37554; MID: 86077733; PMID: 3000440
A;Contents: annotation; gene structure
A;MacGillivray, R.T.; Degen, S.J.; Chandra, T.; Woo, S.L.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 77, 5153-5157, 1980
A;Title: Cloning and analysis of a cDNA coding for bovine prothrombin.
A;Accession: 146045; MUD: 81054926; PMID: 6254059
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 466-599, W, (601-625 < wAz.)
A;Residues: 466-599, W, (601-625 < wAz.)
A;Cross-references: EMBL:V00135; NID:9772; PIDN:CAA23451.1; PID:9808945
B;Pejler, G.; Karlstroem, A.R.; Berg, L.
Eur. J. Blochem. 227, 102-107, 1995
A;Title: Identification of the proteolytic thrombin fragments formed after cleavage w A;Reference number: S67518; WUID:95154277; PMID:7851376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Comment: Thrombin can cleave the amino-terminal activation peptide 1 from prothromb C;Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carb ent interaction with the negatively charged phospholityld membrane surface.
C;Comment: The prothrombin precursor is synthesized in the liver.
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology C;Reywords: blood coagulation; calcium binding; carboxyglutamic acid; duplication; gl F;124/Domain: signal sequence #status predicted F:1-14/Domain: signal sequence #status predicted F:25-43/Domain: Gla domain monlogy 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: profein
A;Molecule type: profein
A;Residues: 318-325,333-338,'X',340;367-374;481-484,'X',486-488;515-522 <PEJ>
A;Residues: 318-325,333-338,'X',340;367-374;481-484,'X',486-488;515-522 <PEJ>
C;Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fil C;Comment: Prothrombin is activated on the surface of a phospholipid membrane that bit tivation peptide and cleaves the remaining part into light and heavy chains. The acti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Magnusson, S.; Sottrup-Jensen, L.; Petersen, T.E.; Claeys, H.
in Boerhaave Symposium on Prothrombin and Related Coagulation Factors, Hemker, H.C.,
A;Reference number: A37552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 44-287,'N',289-352,'E',354,'Q',356-548,'ND',551-599,'N',601-625 <WAG>
A;Note: the evidence for 231-Ser is strong
A;Note: disulfide bonds and carbohydrate binding sites were determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-625 <IRW>
MacGillivray, R.T.A.; Davie, E.W.
Biochemistry 23, 1626-1634, 1984
A:Title: Characterization of bovine prothrombin mRNA and its translation product.
A;Reference number: A00915; MUID:84203525; PMID:6326805
                                                                                                                                                                                                         #text_change 18-Jun-1999
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F;200-317/Domain: activation peptide 2 #status experimental <FR2>
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;44-199/Domain: activation peptide 1 *status experimental <FRI>
                                                                                                                                                                                                                                                                                                                                                                                                             gene.
                                                                                                                                         C; Species: Bos primigenius taurus (cattle)
C; Date: 24-Apr-1984 #sequence_revision 14-Jul-1994 #text_ch
C; Accession: SO2537, A00915; A37552; I46045; S67518
R; Irwin, D.M.; Robertson, K.A.; Macdillivray, R.T.A.
J; Mol. Biol. 200, 31-45, 1988
A; Title: Structure and evolution of the bovine prothrombin A; Reference number: SO2537; MUD:88245190; PMID:3379642
A; Accession: SO2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA
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A;Residues: 1-230,'H',232-625 <
A;Note: 600-Asn was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C42696
thrombin (EC 3.4.21.5) B chain - rabbit (fragment)
C15pecies: Oryctolagus cuniculus (domestic rabbit)
C15pate: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C15Accession: C42696
R15Baffeld, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U S.A. 89, 2779-7783, 1992
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq. A;Recession: C42696; MUID:92212913; PMID:1557383
A;Accession: C42696
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra. A;Molecule type: mRNA
A;Residues: 1-236 CABAN>
A;Cross-references: GB:W81396
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Reywords: hydrolase; serine proteinase
F;1-227/Domain: trypsin.homology (fragment) <FRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:119894; OMIM:176930
A; Map posttion: 11p11-11q12
A; Cross-references: GDB:119894; OMIM:176930
A; Map posttion: 11p11-11q12
C; Superfamily: thrombin; Gla domain homology; Kringle homology; trypsin homology
C; Superfamily: thrombin; Gla domain homology; Kringle homology; trypsin homology
C; Superfamily: thrombin; Gla domain predicted <SIG>
C; Superfamily: thrombin; Gla domain predicted <SIG>
C; Superfamily: thrombin; Gla domain predicted <PRO>
F; 1-24-Domain: signal sequence # status predicted <PRO>
F; 25-43-Domain: gla domain homology <GIA>
F; 28-87-Domain: Gla domain homology <GIA>
F; 28-87-Domain: prothrombin # status experimental <AMT>
F; 44-622/Product: prothrombin # status experimental <AMT>
F; 44-327/Domain: activation peptide # status experimental <ACH>
F; 36-186/Domain: kringle homology <FRR2>
F; 31-391/Domain: kringle homology <FRR2>
F; 328-363/Product: thrombin light chain # status experimental <ACH>
F; 36-622/Product: thrombin light chain # status experimental <ACH>
F; 36-62, 90-103; 108-186; 129-169; 157-181; 213-291; 234-274; 262-286/Disulfide bonds: # status F; 31-407/Disulfide bonds: # status predicted
F; 336-482, 536-550, 564-594/Disulfide bonds: # status predicted
F; 416/Binding site: carbohydrate (Asn) (covalent) # status experimental
F; 568/Active site: Ser # status experimental
F; 568/Active site: Ser # status experimental
A;Cross-references: GB:M33031; NID:g190723; PIDN:AAA60220.1; PID:g190724 C;Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibri C;Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds of an be removed either by factor Xa or thrombin; the cleavage into light and heavy chaiter 314-Arg, are released in natural blood clotting.
C;Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma. C;Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxyglutamyl residues bind calcium ions, result from the carboxyglutamyl charged phospholipid membrane surface.
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85.8%; Score 121; DB 1;

85.00 100.08; Pre

Conservative

Query Match Best Local Similarity Matches 21; Conserv

g

5 YRPDEGKRGDACEGDSGGPFV 25

Mismatches

167 YKPEEGKRGDACEGDSGGPFV 187 셤

Score 117; DB 2; Pred. No. 8.3e-09; 1; Mismatches 0

83.0%; 95.2%;

Query Match 83.0 Best Local Similarity 95.2 Matches 20; Conservative

RESULT

```
t42696
through (EC 3.4.21.5) B chain - Pacific hagfish (fragment)
C;Species: Eptatretus stouti (Pacific hagfish)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C;Accession: 142696
B;Banfield, D.K.; MacGillivray, R.T.A.
B;Banfield, D.K.; MacGillivray, R.T.A.
B;C: Natl. Accession: A42696; MUID:92212913; PMID:1557383
B;Accession: 142696
B;Status: preliminary; not compared with conceptual translation
B;Mesidues: 1-236 CBAN>
B;Cross-references: GB:MB1333
B;Cross-references: GB:MB1333
                                                                                             C; Species: Gekko gecko (tokay)
C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C; Accession: E42696
R; Banfield, D.K.; MacGillivray, R.T.A.
R; Banfield, D.K.; MacGillivray, R.T.A.
A; Title: Partial characterization of vartebrate prothrombin cDNAs: amplification and A; Reference number: A42696; MuID:92212913; PMID:1557383
                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A;Nolecule type: mRNA A;Nolecule type: mRNA A;Residues: 1-235 - CBAN> A;Cross-references: GB:M81392 A;Cross-references: GB:M81392 C;Superfamily: thromblin; Gla domain homology; kringle homology; trypsin homology C;Reywords: hydrolase; serine proteinase F;1-226/Domain: trypsin homology (fragment) <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNAs: amplification and
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Cispecies: Oncorhynchus mykiss (rainbow trout (fragment)

Cispecies: Oncorhynchus mykiss (rainbow trout)

Cispecies: Ostoba May 1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999

Cispecies: Ostoba May 1995 Rainbow 1995 Angles: 1992

A; Raference number: A42696; MulD:9212913; PMID:1557383

A; Accession: G4266

A; Status: preliminary

A; Molecule type: mRNA

A; Mesidues: 1-239 <BAN>

A; Cross-references: GB:M81398; NID:9213486; PIDN:AAA49433.1; PID:9213487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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C;Superfamily: thrombin; Gla domain homology; kringle homology;
C;Keywords: hydrolase; serine proteinase
F;1-226/Domain: trypsin homology (fragment) <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 103; DB 2; I
Pred. No. 7.1e-07;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 100; DB 2;
Pred. No. 1.8e-06;
2; Mismatches 2;
                                                                                       thrombin (EC 3.4.21.5) B chain - tokay (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 70.9%;
1 Similarity 81.0%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.0%;
81.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity ....
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Best Local Similarity
Matches 17; Conserv
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Matches
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C; Species: Gallus gallus (chicken)
C; Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Mar-1999
C; Accession: D42696
R; Banfield, D.K.; Macdillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A; Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq A, Accession: D42696
A; Status: preliminary
A; Status: preliminary
F;214-292/Domain: kringle homology <KR2>
F;318-366/Product: thrombin light chain #status experimental <LGH>
F;318-366/Product: thrombin heavy chain #status experimental <HGH>
F;367-615/Product: thrombin heavy chain #status experimental <HGH>
F;367-616/Domain: trypsin homology <TRX>
F;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;51-66,91.104,109-187,130-170,138-182,214-222,235-275,23-287,339-485,394-410,539-553,571,44,419/Binding site: carbohydrate (Asn) (covalent) #status experimental F;409,465,571/Active site: His, Asp, Ser #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombin (EC 3.4.21.5) B chain - Cynops pyrogastor (fire-bellied newt) (fragment) C; Species: Cynops pyrogastor (fire-bellied newt) C; Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: F4266
R; Banfield, D.K.; MacGillitray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A; Title: Partial characterization of vertebrate prothrombin cDNAs: amplification A; Reference number: A42696; MUD: 92212913; PMID:1557383
A; Note: sequence not
A; Accession: F42696
A; Status: preliminary; nucleic acid sequence not shown; not compared with concept
A; Molecule type: mRNA
A; Molecule type: mRNA
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A.Residues: 1-235 <BANA
A.Residues: 1-235 <BANA
A.Gross-references: GB:M81391
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Reywords: hydrolase; serine proteinase
F;1-226/Domain: trypsin homology (fragment) <TRY>
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Pred. No. 1.4e-07;
0; Mismatches 2;
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Pred. No. 7.1e-07;
2; Mismatches 2;
                                                                                                                                                                                                                                               Score 114; DB 1;
Pred. No. 5.5e-08;
0; Mismatches 1.
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95.2%;
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81.0%;
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Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         556 YRPGEGKRGDACEGDSGGPFV
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                                                                                                                                                                                                                                               Query Match 80.9
Best Local Similarity 95.2
Matches 20; Conservative
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Best Local Similarity 81.0
Matches 17; Conservative
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A; Cross-references: GB:M81395
C; Superfamily: thrombin; Gla d
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F;361-610/Domain: trypsin homology <TRY>
F;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F;51-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-54
F;403,459,565/Active site: His, Asp, Ser *status predicted
                                                                                                                                                                                                                                                                                                                                                                                A, Note: the data were obtained from females resulting from the cross of M. domesticus
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C; Species: Acipenser transmontanus (white sturgeon)
C; Deccise: Acipenser transmontanus (white sturgeon)
C; Deccession: H42696
C; Accession: H42696
R; Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A; Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A; Reference number: A42696; MUID:92212913; PMID:1557383
A; Accession: H42696
A; Molecule type: mRNA
A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A; Molecule type: mRNA
A; Csuperfamily: thrombin; Gla domain homology; kringle homology; trypsin homology C; Keywords: hydrolase; serine proteinase
F;1-226/Domain: trypsin homology (fragment) < TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                   R;Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and A;Reference number: A42696; MUID:92212913; PMID:1557383
A;Recession: A42696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology C; Reywords: blood coagulation; catcium binding; carboxyglutamic acid; glycoprotein; F: 1-44 Domain: signal sequence #status predicted <PRO> F; 25-43 Domain: propeptide #status predicted <PRO> F; 26-88 Domain: Gla domain homology <GLA> F; 28-88 Domain: Gla domain homology <GLA> F; 109-187 Domain: kringle homology <RRI> F; 109-187 Domain: kringle homology <PRO> F; 215-293 Domain: kringle homology <PRO> F; 215-
                                               prothrombin and localization
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                                                                                                                                                                                                                                                                                               A; Cross-references: GB:X52308; NID:g53813; PIDN:CAA36548.1; PID:g53814
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Pred. No. 0.0015;
3; Mismatches 5; Indels
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. 5.9e-05;
2;
    DNA Cell Biol. 9, 487-498, 1990
A;Title: Characterization of the cDNA coding for mouse E
A;Reference number: A35827; MUID:91025551; PMID:2222810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein C (activated) (EC 3.4.21.69) precursor - human N; Alternate names: autoprothrombin IIA; plasma protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 92; DB;
Pred. No. 5.9e-
3; Mismatches
                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain C57BL/6
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61.9%;
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76.2%;
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Best Local Similarity 76.2
Matches 16; Conservative
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Cross-references: GB:M81394
                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-618 <DEG>
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H42696
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A; Residues: 44.58 
A; Residues: 44.58 
A; Residues: 44.58 
A; Residues: 44.58 
A; Mote: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute
B; Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A; Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A; Reference number: A42696; MUID:92212913; PMID:1557383
A; Accession: B42696
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Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr
1-24/Domain: signal sequence fstatus predicted <SIG>
25-43/Domain: propeptide fstatus predicted <PRO>
28-88/Domain: Gla domain homology <GLA>
44-617/Product: prothrombin #status experimental <PMAT>
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C;Species: Mus musculus (house mouse)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 03-May-2002
C;Accession: A35827; A42569: 722081
R;Degen, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pai, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;50,51,58,60,63,64,69,70,73,76,Modified site: gamma-carboxyglutamic acid (Glu) #status
;61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,5
;402,458,564/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X52835; NID:956969; PIDN:CAA37017.1; PID:956970
R;Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.
Endocrinology 126, 167-175, 1990
A;Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.
A;Reference number: A60576; MUID:90091942; PMID:2293980
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology C;Keywords: hydrolase; serine proteinase F;1-226/Domain: trypsin homology (fragment) <TRY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Rattus norvegicus (Norway rat)
C;Daces (Norway 1993 #text_change 03-May-2002
C;Daces (Norway 1993 #sequence_revision 07-May-1993 #text_change 03-May-2002
C;Daces (No. 10511, Monard, D. R;Dihanich, M.; Monard, D. Nucleac Acids Res. 18, 4251, 1990
Nucleac Acids Res. 18, 4251, 1990
A;Title: CDNA sequence of rat prothrombin.
A;Reference number: S10511; MUID:90332426; PMID:2377469
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                       Length 239
                                                                                                                                                                                                                                                    2; Indels
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Pred. No. 5.9e-05;
3; Mismatches 2;
                                                                                                                                                                  Score 99; DB.2; Pred. No. 2.6e-06;
                                                                                                                                                                                                                                                        2; Mismatches
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S10511
thrombin (EC 3.4.21.5) precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                 5 YKPDEGKRGDACEGDSGGPFV 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 76.2%;
Matches 16; Conservative
                                                                                                                                                              Query Match 70.2%;
Best Local Similarity 81.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombin (EC 3.4.21.5) precursor
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Molecule type: mRNA
Residues: 383-617,'E' <BAN>
Cross-references: GB:M81397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-617 <DIH>
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C; Accession: S32794
R; Ikeda, M.; Yaginuma, T.; Kobayashi, M.; Yamashita, O.
Comp. Biochem. Physiol. B 99, 405-411, 1991
A; Title: CDNA cloning, sequencing and temporal expression of the protease responsible A; Reference number: S32794; MUID: 92111263; PMID:1764920
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                                            (partial) #status atypical
                                                                                                                                                                                                                                                                                                                                                                                                                                trypsin-like proteinase (EC 3.4.21.-) - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 07-Dec-1994 #sequence_revision 01-Sep-1995 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Homo sapiens (man)
C; Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 19-May-2000
C; Accession: $4536; M.
R; Dihanich, M.; Spiess, M.
Biochim. Biophys. Acta 1218, 225-228, 1994
A; Title: A novel serine proteinase-like sequence from human brain.
A; Reference number: $45356; MUID: 94289486; PMID: 8018728
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A;Experimental source: Alzhelmer's disease patient brain cortex
                                                                                                                                                                       Gaps
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                                                                                                        Length 461;
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               Ser #status predicted
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Pred. No. 0.024;
2; Mismatches 2;
                                                                                                        DB 1;
0.035;
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0.063;
         F;253,299,402/Active site: His, Asp, Ser #status p
F;371/Binding site: carbohydrate (Asn) (covalent)
                                                                                                     Score 71; DB 1
Pred. No. 0.035
0; Mismatches
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Pred. No. 0.063
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: trypsin; trypsin homology C;Keywords: hydrolase; serine proteinase F;28-248/Domain: trypsin homology <TRY>
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                                                                                                        50.4%;
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Best Local Similarity 64.0%
Matches 16; Conservative
                                                                                        Ouery Match
Best Local Similarity 81.2
Watches 13; Conservative
                                                                                                                                                                                                                                                            392 GDRODACEGDSGGPMV 407
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C;Species: Homo sapiens (man
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A; Residues: 1-264 <IKE>
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A; A; Status: preliminary
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S00845
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J. Biol. Chem. 255, 11397-11404, 1990
J. Biol. Chem. 255, 11397-11404, 1990
J. Milettch, J.P.; Broze Jr., G.J.
J. Biol. Chem. 255, 11397-11404, 1990
J. Mill. Special of the state of translation in A.Reference number: A44605; MUID:90293094; PMID:1694179
A.Contents: annotation; carbohydrate binding sites; activation peptide
A.Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not R.Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A.Sontents: annotation; beta-hydroxyaspartic acid
A.Reference number: A44606; MUID:92184750; PMID:1544894
A.Contents: annotation; beta-hydroxyaspartic acid
C.Comment: Protein C is the zymagen of the vitamin K-dependent serine proteinase that in Ivation of factor vals strongly enhanced by complexing with protein C also forcomment: Protein C is synthesized in the liver as a single chain precursor, which is of the which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212-445/Domain: trypsin homology <TRY>
48,49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp
59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/q
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A; Residues: 'Q', 107-461 <FOS2>
A; Cross-retences: GB: KO2059; NID: g190322; PIDN: AAA60164.1; PID: g190323
A; Cross-retences: GB: KO2059; NID: g190322; PIDN: AAA60164.1; PID: g190323
B; Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutzky, J.; Crabtree, G.R.; Long, G.L.
Nucleic Acids Res. 13, 5233-5247, 1985
Nucleic Acids Res. 13, 5233-5247, 1985
A; Title: The structure and evolution of a 461 amino acid human protein C precursor and i
A; Reference number: A23789; MUID: 85269639; PMID: 2991859
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1:13/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:139, 290, 355/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;211-212/Cleavage site: Arg-Leu (trombin) #status experimental
A;Accession: A25426
A;Molecule type: DNA
A;Residues: 1-445,'L','446-461 <PLU>
A;Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332
                                                                                                                                                                                                                                                   A;Molecule type: DNA
**Residues: 1-461 <FROSI>
A;Cross-references: GB:Mil228; NID:g190333; PIDN:AAA60166.1; PID:g190334
A;Cross-references: GB:Mil228; NID:g190333; PIDN:AAA60166.1; PID:g190334
R;Plutzky, J; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
R;Plutzky, J; Hoskins, J.A.; S66-S56, 1986
A;Fitle: Bvolution and organization of the human protein C gene.
A;Reference number: A25426; MUID:86120978; PMID:3511471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;MOlecule type: mRNA
A;Residues: 1.461 <BEC>
A;Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
                                                                                        Rifoster, D.C.; Yoshitake, S.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
A;Title: The nucleotide sequence of the gene for human protein C.
A;Reference number: A22331; MUID:85270390; PMID:2991887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Foster, D.; Davie, E.W.

roc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984

:Title: Characterization of a cDNA coding for human protein C.; Reference number: A21781; MUID:84272714; PMID:6589623

Accession: A21781
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         C; Species: Homo sapiens (man)
                                                                                                                                                                                                                      A; Accession: A22331
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Riceytus, S.P.; Lob, K.R.; Hagen, F.S.; Kurachl, K.; Davle, E.W.
Blochemistry 27, 1067-1074, 1988
A;Title A novel trypsin-like serine protease (hepsin) with a putative transmembrane dom A;Reference number: S00845; MUID:88209431; PMID:2835076
A;Accession: S00845
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A;Residues: 1-417 <LEF>
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A;Cross_references: EMBL:X07732; NID:932063; PIDN:CAA30558.1; PID:932064
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB: HPN; TMPRSS1; hepsin
A; Cross-references: GDB:135685; OMIM:142440
A; Map position: 1941-119413.2
C; Superfamily: hepsin; trypsin homology
C; Keywords: hydrolase; llver; serine proteinase; transmembrane protein
F; 23.45.Domain: transmembrane #status predicted <TMN>
F; 165-400/Domain: trypsin homology <TRY>
F; 168-204,291-359,322-338,349-381/Disnifide bonds: #status predicted
F; 108-204,291-359,322-338,349-381/Disnifide bonds: #status predicted
F; 203,257,353/Active site: His, Asp, Ser #status predicted
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Matches 15; Conserva
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Search completed: May 12, 2003, 15:39:44 Job time: 28.5 secs

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us-09-909-348-5.rsp

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 12, 2003, 15:32:07 ; Search time 14.5 Seconds (without alignments) 71.511 Million cell updates/sec

US-09-909-348-5 141 1 AGTRIKPDEGKRGDACEGDSGGPFV 25

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum.Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	P00734 homo sapten	_		P19221 mus musculu	Q28506 macaca mula	P04070 homo sapien	Q07943 bombyx mori	_	Q9bqr3 homo sapien	_		_	P05981 homo sapien	homod	3 canis	capra	028412 felis silve	-		Q9er04 mus musculu	Q9h3s3 homo sapten		homo	homo	8 13 8	P00745 bos taurus	bos t		drosc	P54627 drosophila	พกร น	2 homo	Q9p0g3 homo sapien
TD QI	THRB HUMAN	THRB_BOVIN	THRB_RAT	THRB_MOUSE	PRTC_MACMU	PRTC_HUMAN	VDP_BOMMO	TRYZ_DROER	MPN_HUMAN	PRTC_RABIT	KLKF_HUMAN	HEPS_MOUSE	HEPS_HUMAN	KLKD_HUMAN	PRTC_CANFA	PRTC_CAPHI	PRTC_FELCA	PRTC_HORSE	TRY3_ANOGA	TMS5_MOUSE	TMS5_HUMAN	PRTC_PIG	DES1_HUMAN	CFAD_HUMAN	CFAD_PIG	PRTC_BOVIN	TPA_BOVIN	NETR_HUMAN	NDL_DROME	TRYE_DROER	PRIC_MOUSE	FA10_HUMAN	KLKE_HUMAN
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MEDLINE-93043342; Pubmed-1421398;
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                                                                                                                                                thrombin.
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ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
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MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
MISCELLANEOUS: THE AMINO END OF PROTHROMBIN &
PACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
                                                                                                                                                                                                                             "Prothrombin Salakta: substitution of glutamic acid-466 by alanine reduces the fibrinogen clotting activity and the esterase activity."; Blochemistry 31:7457-7462(1992).
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MISCELLANDOUS: THROMEIN CAN ITSELE CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Detection of a single base substitution of the gene for prothrombin Tokushima. The application of PCR-SSCP for the genetic and molecular analysis of dysprothrombinemia."; Int. J. Hematol. 55:93-100(1992).
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Míyata T., Morita T., Inomoto T., Rawauchi S., Shirakami A.,
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MEDLINE-92256895; Pubmed-1349838;
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                                                                                                VARIANT SALAKTA.
MEDLINE-92378975;
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MEDLINE-92218459; PubMed-1560020;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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MEDLINE-91311686; PubMed-1856869;
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                   Length 622;
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                                      2.6e-09;
                     DB 1;
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01-ARR-1990 (Rel. 14, Last sequence update)
02-JUN-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.21.5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 23:1626-1634(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 25:3977-3982(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Biol. 220:481-494(1991).
                                                                                                                     553 YKPDEGKRGDACEGDSGGPFV 573
                                                                                                  YKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biol. 200:31-45(1988)
                                                       Conservative
                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                         taurus (Bovine)
              Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resolution.
                                                                                                                                                                                                                                           THRB_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product
                                                                                                                                                                                                                        THRB_BOVIN
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                                                                                                                                                                                                     RESULT 2
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MEDLINE-8607733; Pubmed-3000440;

RA ITWIN D.M., Ahern K.G., Pearson G.D., McGillivray R.T.A.;

I'Characterization of the bovine prothrombin gene.";

Blochemistry 24:6854-6861(1985).

LI BLOCHAMISTRY 24:6854-6861(1985).

-I- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS

TEIBRINGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,

AND, IN COMPLEX WITH THROMBONDOULD, PROTEIN C.

-I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Gly; activates

-I- STRUCELLULAR LOCATION: Extracellular.

-I- TISSUE SPECIFICITY: SYWTHESIZED IN THE LIVER; FOUND IN PLASMA.

-I- TISSUE SPECIFICITY: SYWTHESIZED IN THE LIVER; FOUND IN PLASMA.

-I- PTM: THE GAMMA-CARBOXYLGUTAMYL RESIDUES WITH MIND ARGASOMAL

REGULT FROM THE CARBOXYLGUTAMYL RESIDUES BY A MICROSOMAL

REGULT FROM THE CA-DEPENDENT CARBOXYLARE. THE MODIFIED RESIDUES

ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY

CHARGED PHOSPHOLIPID SHURFOWNIN IS ESSENTIAL FOR THE CONVERSION

COF PROTHROMBIN TO THROMBIN.

-I- MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A PROSPHOLIPID MEMBRANE THAT BINDS THE REMAINING PART INTO LIGHT FACTORS AS REMOVES

THE ACTIVATION PEPTIDE & CLEAVES STARTS SLOWIX BECAUTE FACTOR

HENCY CHARLEL HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF

HENCHMAN AND ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.
MEDLINE-97102783; PubMed-8947023;
van de Locht A., Stubbs M.T., Bode W., Friedrich T., Bollschweller C.,
Brandstetter H., Turk D., Hoeffken H.W., Grosse D., Stuerzebecher J., Martin P.D., Edwards B.F.P., Bode W.; Refined 2.3 A X-ray crystal structure of bovine thrombin complexes formed with the benzamidine and arginine-based thrombin inhibitors NAPAP, 4-TAPAP and MOPA. A starting point for improving antithrombotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huber R., Bode W.; "Structure of the thrombin complex with triabin, a lipocalin-like exosite-binding inhibitor derived from a triatomine bug."; Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuentes-Prior P., Noeske-Jungblut C., Donner P., Schleuning W.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The ornithodorin-thrombin crystal structure, a key to the TAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF COMPLEX WITH TRIABIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY FACTOR XA.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
DATABASE: NAME-ProZyme technical fact sheet;
WWW-"http://www.prozyme.com/technical/thrombindata.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                                                                                                                                                                                Mol. Biol. 226:1085-1089(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98004486; PubMed-9342325;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO J. 15:6011-6017(1996).
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PDB; 1ETR; 31-JAN-94
PDB; 1ETS; 31-JAN-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huber R.
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PIR; S02537; S02537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoffken W.,
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556 YKPGEGKRGDACEGDSGGPFV 576
                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HROMBIN.
                                                                                                                                                                                                                                                     TISSUE-Liver;
                                                                    01-NOV-1990
                                                                             01-NOV-1990
15-JUN-2002
                                                 THRB_RAT
 셤
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                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50240; TRYPSIN_DOM: 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_BIS; 1.
BLOOD COSQUILATION: Plasma; Calcium-binding; Glycoprotein; Repeat; Vitamin R; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver; Hydrolase; Serine protease; Kringle; Signal; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVATION PEPTIDE (FRAGMENT 1)
ACTIVATION PEPTIDE (FRAGMENT 2)
THROMBIN LIGHT CHAIN (A).
THROMBIN HEAVY CHAIN (B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 114; DB 1; Length 62
Pred. No. 2.4e-08;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAMMA-CARBOXYGLUTAMIC
GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAMMA-CARBOXYGLUTAMIC GAMMA-CARBOXYGLUTAMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAMMA - CARBOXYGLUTAMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTHROMBIN.
                                                                                                                                                                                                                                                                                                         Tryp_SPc; 1.
1; GLU_CARBOXYLATION; 1.
1; KRINGLE_1; 2.
1; KRINGLE_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRINGLE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRINGLE 2
                                                                                                                                                                             InterPro; IPR003966; Prothrombin:
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                   Chymotrypsin.
                                                                                                                                                           nterPro; IPR002383; GLA_blood.
nterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                          CHYMOTRYPSIN
                                                                                                                                                                                                                                                                      R01505; PROTHROMBIN.
D0000395; Kringle; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.9%;
llarity 95.2%;
Conservative
                                                                                                                                                                                                                                                   GLABLOOD.
                                                                                                                                                                                                                   PF00089; trypsin; 1.
PF00594; gla; 1.
                                                                                                                                                                                                                                                               ; KRINGLE
                                                                                                                                                                                                           1; kringle;
                                                                                                                    17-JUN-98.
16-FEB-99.
                                                                                                                                                  InterPro; IPR001314;
                                                                                                         06-MAY-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match.
Best Local Similarity
Matches 20; Conserv
                                        - MAY-
                                                                                                                                                                                                                                                                                                                                           PS50070;
                                                                                                                                                                                                                                           RINTS; PR00722;
                                                                                                                                                                                                                                                                      PRINTS; PR01505
                                                                                                                                                                                                          fam; PF0005
                                                                                                                                        MEROPS; S01
                                                                                                                    1AOH;
1AVG;
                                                 1MKW;
                                                                     LTBO
                             PF2
                                     SPT
                                                                                                                                                                                                                                                                                           SMART; SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                           ROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
PEPTIDE
                                                                                                                                                                                                                                                                                 roDom;
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MOD_RES
MOD_RES
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                        ROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                       fam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                          PDB;
                                    PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
                                                                                                                              DB;
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RA Banfield D.K., Macgillivray R.T.;

**Partial characterization of vertebrate prothrombin cDNAs:

**Partial characterization of vertebrate prothrombin cDNAs:

**Partial characterization of vertebrate prothrombin from amplification and sequence analysis of the B chain of thrombin from the different species.";

**Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).

**C. T. CAPALYTON: THROMBONDILIN, PROTEIN C.

**C. T. CAPALYTIC ACTIVITY: Preferential cleavage: Arg-1-Gly: activates fibrinogen to fibrin and releases fibrinopeptide A and B.

**C. T. PTM: THE GAMMA-CARBOXYLATION OF GLUTAMYL RESIDUES WA MICCHSONAL RESIDUES WA WHICH BIND CALCIUM IONS, RESULT FROM THE CA-DEPENDENT INTERACTION WITH A NEGALIVELY CRARACTED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION CONVENSION CONFORMANCE THE MAINT INTERACTIONS; FACTOR A REMOVES THE ACTIVATION PROCESS STARTS SLOWIX BRCAUGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWIX BRCAUGE FACTOR MUCHEN AND A PROCESS STARTS SLOWIX BRCAUGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWIX BRCAUGHT & HEAVY CHAINS. THE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF THE MADUNTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                     Fattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
                                                                                                                                                                             01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (BC 3.4.21.5).
                                                                       617 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley, TISSUE-Liver;
MEDLINE=90332426; PubMed=2377469;
Dibanich M., Monard D.;
"cDNA sequence of rat prothrombin.";
Nucleic Acids Res. 18:4251-4251(1990).
                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chymotrypsin.
GLA_blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92212913; PubMed-1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kringle.
Prothrombin
                                                                                                                                               (Rel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE OF 383-617 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X52835; CAA37017.1; -. EMBL; M81397; AAA42240.1; -. PIR; S10511; S10511. S10511. HSSP: P00734; 1UVS. MEROPS; S01.217; -.
                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001314;
InterPro; IPR002383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000001;
InterPro; IPR003966;
RESULT 3
THRB RATE 11D PT 182 PAR 182
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STANDARD;

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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                         Friezner Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G., Fitzgibbon J.J., Pal J.-A., Chapman V.M., Elliott R.W.; "Charcterization of the cDNA coding for mouse prothrombin and localization of the gene on mouse chromosome 2."; DNA Cell Biol. 9:487-498(1990).
                                                                                                          01-NoV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UNY-2002 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.11.5).
                                                                                                                                                                                                                                                                                                        STRAIN-C57BL/6; TISSUE-Liver;
MEDLINE-91025551; PubMed-2222810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 384-618 FROM N.A.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PISSUE=Liver;
                                                                           THRB_MOUSE
                                                          THRB_MOUSE
                                                                                             acid; Acute phase; Liver;
                                                                                                                                                                                                                                         PROSITE; PS00021; KRINGLE_1; 2.
PROSITE; PS50070; KRINGLE_2; 2.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat; Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Live Hydrolase; Serine protease; Kringle; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATION PEPTIDE (FRAGMENT 1).
ACTIVATION PEPTIDE (FRAGMENT 2).
THROMBIN LIGHT CHAIN (A).
THROMBIN HEAVY CHAIN (B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.2%; Score 92; DB 1; Length 617; 76.2%; Pred. No. 2.5e-05; 1ve 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (GLCNAC. ..)
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GAMMA-CARBOXYGLUTAMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                               PROTHROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRINGLE 1.
KRINGLE 2.
                                                                                                                                                                                                               SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
InterPro; IPR001254; Ser_protease_Try
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00051; Kringle; 2.
Pfam; PF00069; 'trypsin; 1.
Pfam; PF00594; gla; 1.
                                                                                PRINTS, PRO0722, CHYMOTRYPSIN.
PRINTS, PRO0001, CLABLOOD
PRINTS, PRO0018, KRINGLE.
PRINTS, PRO1505, PROTHROMBIN.
PRODOM; PD000395, KIINGLE, 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70411 MW;
                                                                                                                                                          ProDom; PD000395; Krin
SMART; SM00069; GLA; 1
SMART; SM00130; KR; 2.
SMART; SM00020; Tryp_S
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617 AA;
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Best Local Simi
Matches 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
BY FACTOR XA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002383; GLA_blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X52308; CAA36548.1; -..
EMBL; M81394; AAA40435.1; -.
PIR; A35827; A35827.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       THROMBIN.
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Gaps

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569

549

YKPDEGKRGDACEGDSGGPFV 25

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Conservative

Similarity

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PROSITE:
PRO
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KRINGLE 2.

SERING 2.

SERING PROTEASE.

CLEAVAGE (BY THROMBIN).

CLEAVAGE (BY FACTOR XA).

CLEANGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

GRANG RELAY SYSTEM (BY SIMILARITY).

GRANA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGLUTAMIC ACID.
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ACTIVATION PEPTIDE (FRAGMENT 2)
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BY SIMILARITY.
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N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
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                                                                                                                                                                                                                                                                                                                                                                                   400020; Tryp_SPc; 1.
PS00011; GLU_CARBOXYLATION; 1.
PS00021; KRINGLE_1; 2.
                                                  InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF000051; kringle; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF000894; gla; 1.
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InterPro; IPR000001; Kringle.
InterPro; IPR003966; Prothrombin.
                                                                                                                                                                                        PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
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PRINTS; PR01505; PROTHROWBIN.
PRODOM; PD000395; Kringle; 2.
SMART; SM00069; GLA; 1.
SMART; SM00130; KR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       553
618 AA;
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MOD_RES
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MEDLINE-94318474; PubMed-8043441;
Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2004 (Rel. 41, Last annotation update)
15-UN-2004 (Rel. 41, Last annotation update)
16-UN-2004 (Rel. 41, Last annotation update)
17-UN-2004 (Rel. 41, Last annotation update)
18-UN-2004 (Rel. 41, Last annotation update)
18-UN-2004 (Rel. 41, Last annotation update)
18-UN-2004 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalla; Butherla; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
N'LINKED (GLCNAC. .) (POTENTIAL)
N'LINKED (GLCNAC. .) (POTENTIAL)
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PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1.
Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17770 MW; 27D78F185B2FCC69 CRC64;
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Pred. No. 0.0053;
); Mismatches 3;
                                                         161 AA
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HSSP; P04070; 1PCU.
MEROPS; S01.218; --
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPC; 1.
                                                            PRT;
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                                                            STANDARD;
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Q28506;
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RESULT 5
PRTC_MACMU
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3;

Conservative

16;

Similarity

65.2%;

PRTC_HUMAN

RESULT 6

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Gaps

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Length 618;

EMBO J. 15:6822-6831(1996).

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P04070; Q16001; Q15190; Q15189;
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15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C precursor (EC 3.4.21.69)
(Autoprofirembin IIA) (Anticoagulant protein C) (Blood coagulation
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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Busaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cysteine sites.";
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SEQUENCE OF 106-461 FROM N.A.
MEDLINE=84272714; PubMed=6589623;
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MEDLINE-86120978; Pubmed-3511471;
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MEDLINE-93250852; PubMed-1301959;
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MEDLINE-92380660; Pubmed-1511988;
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Hum. Genet. 89:683-684(1992)
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MEDLINE-90098906;
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                    VARIANT SER-334.
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MEDLINE-94122329; PubMed-8292730;
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MEDLINE-93313192; PubMed-8324221;
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lood Coagul. Fibrinolysis 4:345-347(1993).
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MEDLINE-94001606; PubMed-8398832;
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Mutat. 1:491-500(1992).
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                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                              Ikeda M., Yaginuma T., Kobayashi M., Yamashita O.; "cDNA cloning, sequencing and temporal expression of the protease responsible for vitellin degradation in the silkworm, Bombyx mori."; Comp. Blochem. Physiol. 99B:405-411(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPHA-VTN PROTEASE CHAIN 1 (POTENTIAL).
ALPHA-VTN PROTEASE CHAIN 2 (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
       Hexapoda;
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda
Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
Ditrysia; Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       · · · ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATION PEPTIDE (POTENTIAL). BETA-VIN PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zymogen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6D536DD4184123AF CRC64;
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CHARGE RELAY SYSTEM (BY S
SUBSTRATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 70.5; DB 1;
Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> T (IN REF. -> S (IN REF. -> T (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dENVES; SYLLEY CHAMOLIYPSIN.
InterPro; IPR001134; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Serine protease; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 AGT---PEGGK--DACQGDSGGPLV 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGTRYKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                        STRAIN-N4; TISSUE-Egg;
MEDLINE-92111263; PubMed-1764920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00020; Tryp_SPc; 1.
SMOSITE; PSS0240; TRYPSTR_DOM; 1.
PROSITE; PS00134; TRYPSTR_HS; 1.
PROSITE; PS00135; TRYPSTR_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28521 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D16232; BAA03757.1; -. EMBL; D16233; BAA03758.1; -. PIR; S32794; S32794; HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 64.0
nes 16; Conservative
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161
251
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                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.113;
                                                                     NCBI_TaxID=7091;
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P54630;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vitamin-K dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).
                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
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SIMILARITY).
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBL_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
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N'LINKED (GLCNAC. . ) (POTENTIAL).
N'LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                 SECTENCE FROM N.A. FORWIINGS N.D., Barrett A.J.; Fortunato M., Dando P.M., Rawlings N.D., Barrett A.J.; "Cloning, sequencing and expression of marapsin, a human serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; DB 1; Length 290; 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                     Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINKED (GLCNAC. . .) (PO 67BDC93EC70BFF7B CRC64;
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(BY
(BY
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CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SERINE PROTEASE
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68.5;
                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO 19F001314; Chymotrypsin.
InterPro: IPR001254; Ser_protease_Try.
Pram: PP00089; trypsin, 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM0020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_HS; 1.
PROSITE; PS00134; TRYPSIN_HS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
Marapsin precursor (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31940 MW;
                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ306593; CAC35467.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 DEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                Homo saptens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; S01.074;
                                                                                                                                                                        proteinase."
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Q28661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
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ACT_SITE
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CARBOHYD
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Matches
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.

REQUIRED FOR SPECIFICITY (BY SIMILARITY).
Aleobel812AAD468 CRC64;
                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropóda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                      ACTIVATION PEPTIDE.
TRYPSIN ZETA.
TRYPSIN SETA.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001314; Chymotrypsin,
InterPro; IPR001334; Ser_protease_Try.
Ffam; PF00089; trypsin; 1.
FRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00020; Tryp_SPC; 1.
SWART; SR00134; TRYPSIN_HIS; 1.
FROSITE; PS00134; TRYPSIN_HIS; 1.
FROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Zymogen; Signal; Multigene family.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.6%; Score 70; DB 1; 70.0%; Pred. No. 0.012; tive 1; Mismatches
                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trypsin zeta precursor (EC 3.4.21.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0015083; Dere\Try-zeta.
                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29735 MW;
                                                                                                                                                                                 Drosophila erecta (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 GKRGVGGADACQGDSGGPLV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U40653; AAA83236.1; -. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 GKRG----DACEGDSGGPFV 25
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                                                              STANDARD;
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281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.112;
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16-OCT-2001 (
15-JUN-2002 (
                                                                FRYZ DROER
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MPN_HUMAN
ID MPN_HUMAN
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ACT_SITE
DISULFID
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PROPEP CHAIN

Q9BQR3;

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51087 MW;
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                               52
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250
250
296
399
105
1105
1114
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                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                         26
                                                                                                                                     9
                                                                                                                                                          2007
2008
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2008
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2008
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KLKF_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                   SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE BNIZME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO BIN OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBONDULLING.
                           TISSUE SPECIFICATY: PLASMA; SYNTHESIZED IN THE LIVER.

PTM: THE VITAMIN R-DEPENDENT, ENZIMATIC CARBOXILATION OF SOME
EDG RELIONS THE MODIFIED FROTEIN TO BIND CALCIUM.

MISCELLANBOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFIXITY TO

ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
SITE IS NECESSARY FOR THE RECCGNITION OF THE
THROMBIN-THROMBOMODULIN COMPLEX.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blood coagulation; Glycoprotein; Serine protease; Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation; EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal. NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
VITAMIN K-DEPENDENT PROTEIN C.
PROTEIN C LIGHT CHAIN (BY SIMILARITY).
PROTEIN C HEAVY CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERINE PROTEASE.
GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001881; EGE_Ca.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSO1186; EGF.2; 2.
PROSITE; PSO1187; EGF.CA; 1.
PROSITE; PSO0011; GLC.CARBOXXLATION;
PROSITE; PSO0134; TRYPSIN_HCS; 1.
PROSITE; PSO0134; TRYPSIN_HCS; 1.
                                                                                                                                                                                                                                                                                                                                                                                        interPro; IPR000152; Asx_hydroxyl.
interPro; IPR000561; EGF-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00020; TYP_SPC: 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00022: EVE
                                                                                                                                                                                                                                                                                                                                                       EMBL; U49933; AAA92956.1; -. HSSP; P04070; 1PCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00594; gla; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00181; EGF;
SMART; SM00069; GLA;
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              MEROPS; S01.218
                       rissue-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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Gaps
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Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed-11010966;
Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.P.;
Wholecular cloning of the human kallikrein 15 gene (KLK15). Upregulation in prostate cancer.";
J. Biol. Chem. 276:53-61(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó;
                                                                                                                                                                                                                                                    (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY)
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                      ĠAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                           GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                   GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                               (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D75A5F990C8F29D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Kallikrein 15 precursor (EC 3.4.21.-) (ACO protease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OGHARS, OGHARS, OGHARS, OGHARS, 16-OCT-2001 (Page 10-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 68; DB 1;
Pred. No. 0.038;
                                                                                                                                        (BY SIMILARITY).
                                                          BY SIMILARITY)
                                                                                                 BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Serine protease; Transmembrane; Signal-anchor.

CHAIN 162 416 CATALYTIC CHAIN (POTENTIAL).

CATALYTIC CHAIN (POTENTIAL).

CATOPLASMIC (POTENTIAL).

TRANSMEM 17 43 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

(POTENTIAL).
                                                                                                                                                                                            MEDILINE-98058912; PubMed-9395459;
Vu T.-K.H., Liu R.W., Haaksma C., Tomasek J.J., Howard E.W.;
"Identification and cloning of the membrane-associated serine
procease, hepsin, from mouse preimplantation embryos.";
J. Biol. Chem. 272:31315-31320(1997).
-: FUNCTION: PLAYS AN ESSENTIAL ROLE IN CELL GROWTH AND MAINTENANCE
                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 67; DB 1; Length 416; Pred. No. 0.047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POT
N; 432194Ff4004F848 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                          1- SUBCELLULAR LOCATION: Type II membrane protein.
1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417 AA.
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InterPo; IPR001314; Chymctrypsin.
InterPo; IPR001314; Chymctrypsin.
InterPro; IPR001364; Scr_receptor.
InterPro; IPR001190; Src_receptor.
Pfam; PF00089; trypsin; 1.
SWART; SW00722; SR; 1.
SWART; SW00202; SR; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00114; TRYPSIN_BIS; 1.
PROSITE; PS001135; TRYPSIN_BER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 GNQIKPKMFCAGYPEGGIDACQGDSGGPFV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GTRYKPDEGKRG-----DACEGDSGGPFV 25
Serine protease hepsin (EC 3.4.21.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF030065; AAB84221.1; -.
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P05981;
01-NOV-1988 (Rel. 09, Created)
                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44739 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 47.5%;
Local Similarity 50.0%;
hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                          OF CELL MORPHOLOGY
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                                                                                                            NCBI_TaxID-10090;
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DISULFID
DISULFID
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CARBOHYD
SEQUENCE
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                         SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y SIMILARITY).
Y SIMILARITY).
(POTENTIAL).
(POTENTIAL).
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CHARGE RELAY SYSTEM (BY SIMILARITY),
CHARGE RELAY SYSTEM (BY SIMILARITY),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN ISOFORM 3).
SHNEPGTAGSPRSQ -> PLSSP (IN REF. 2).
B5EBF8D6022786B5 CRC64;
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KALLIKREIN 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEGM; PF00089; LTYPSIN; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMORO20; TTYP_SPC; 1.
PROSITE; PS50240; TTYPSIN_DOM; 1.
PROSITE; PS00146; TRYPSIN_BIS; 1.
PROSITE; PS00135; TRYPSIN_BIS; FALSE_NEG.
Hydrolase; Serine protease; Glycoprotein; Signal; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
MISSING (IN ISOFORM 4)
MISSING (IN ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V -> G (IN ISOFORM 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 67; DB 1;
Pred. No. 0.029;
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(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
           PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X75363; CAA53145.1; ALT_SEQ
                                                          MEDLINE-94289486; PubMed-8018728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF242195; AAG09469.1; -.
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EGRGAESCEGDSGGPLV 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ternative splicing
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .081;
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15-JUL-1998
15-JUL-1998
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEPS_MOUSE
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CONFLICT
SEQUENCE
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Gaps

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RESULT 12 HEPS_MOUSE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine protease; Transmembrane; Signal-anchor.

1 162 NON-CATALYTIC CHAIN (POTENTIAL).

1 17 CATALYTIC CHAIN (POTENTIAL).

1 17 CYTOPLASMIC (POTENTIAL).

1 17 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
01-NOV-1988 (Rel. 09, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine protease hepsin (EC 3.4.21.-) (Transmembrane protease, serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammalian cell growth.";
Proc. Natl. Acad. Sci. U.S.A. 90:7181-7187(1993).
-1- FUNCTION: PLAYS AN ESSENTIAL ROLE IN CELL GROWTH AND MAINTENANCE
                                                                                                                                                                                                                                                                                   Leytus S.P., Loeb K.R., Hagen F.S., Kurachi K., Davie E.W.;
An Ovole Lrypsin-like serine protease (hepsin) with a putative
transmembrane domain expressed by human liver and hepatoma cells.";
Blochemistry 27:1067-1074(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93348237; PubMed-8346233;
Torres-Rosado A., O'Shea K.S., Tsuji A., Chou S.H., Kurachi K.;
"Hepsin, a putative cell-surface serine protease, is required for
                                                                                                                              Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91358502; Pubmed-1885621;
Tsuji A., Torres-Rosado A., Arai T., le Beau M.M., Lemons R.S.,
Chou S.H., Kurachi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Hepsin, a cell membrane-associated protease. Characterization,
tissue distribution, and gene localization.";
J. Biol. Chem. 266:16948-16953(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEVEL IN LIVER.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001190; Srcr_receptor.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00202; SR; 1.
SMART; SM00202; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LS; 1.
                                                                                                                                                                                                                                        TISSUE=Liver;
MEDLINE=88209431; PubMed=2835076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M18930; AAA36013.1; -. EMBL; X07732; CAA30558.1; -. EMBL; X07002; CAA30058.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S00845; S00845.
HSSP; P00763; IDPO.
MEROPS; S01.224; -.
Genew; HGNC:5155; HPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF CELL MORPHOLOGY
                                                                                                              sapiens (Human).
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
                                                                                                                                                                           NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45
                                                                                          TMPRSS1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
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DOMAIN
                                                                                                                Ношо
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Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Banganan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,

Andreise T., Trankhelm M., Attix C., Amico-Keller G., Coefield J.,

Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,

Arellano A., Sanders C., Ow D., Nolan M., Trong S., Robayashi A.,

Glsen A.S., Carrano A.V.;

"Sequence analysis of chromosome 19q13.4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-20229789; PubMed-10766816;
Yousef G.M., Chang A., Diamandis E.P.;
"Identification and characterization of KLK-L4, a new kallikrein-like
"gene that appears to be down-regulated in breast cancer tissues.";
J. Biol. Chem. 275:11891-11898(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ansorge W., Wirkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: Secreted (Probable).
---- TISSUE SPECIFITY: EXPRESSED IN PROSTATE, BREAST, TESTIS AND SALIVARY GLAND.
----- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 [Rel. 40, Created)
16-OCT-2001 [Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-like protein 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLK13 OR KLKL4.
Momo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
                                                                                                                                                                                             .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                         ;
9
                                                                                                                                                                                                                                                                                 Length 417;
                                                                           INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POT!
                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                    B2086FF661E551D7 CRC64;
                                                                                                                                                                                                                                                                              DB 1;
0.047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 AA
                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                              Score 67;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                          329 GNQIKPKMFCAGYPEGGIDACQGDSGGFFV 358
                                                                                                                                                                                                                                                                                                                                                                                          2 GTRYKPDEGKRG-----DACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF135024; AAD26425.2; -.
EMBL; AC011473; AAG23259.1; -.
EMBL; AL050220; CAB43320.1; ALT_INIT.
                                                                                                                                                                                                                          45011 MW;
                                                                                                                                                                                                                                                                           47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-180 FROM N.A.
                                                                                                                                                                                                                                                                                                                                      15; Conservative
203
257
277
277
204
338
311
                                                                                                                                                                                                                    417 AA;
                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9Y433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Uterus
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                                                                                                                                   DISULFID
DISULFID
CARBOHYD
ACT_SITE
ACT_SITE
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DISULFID
                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                              Local
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Matches
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                    Blood coagulation; Glycoprotein; Serine protease; Hydrolase.
                                                                                                                                                                                                                                                                                Score 65; DB 1; Length 157;
Pred. No. 0.035;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                       E8B1BACF49220DFB CRC64;
                                                    InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1,
SMARY; SM00020; Tryp_SPc; 1,
PROSITE; PS50240; TRYPSIN_DOM; 1,
PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1,
                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: May 12, 2003, 15:36:42
Job time : 15.5 secs
                                                                                                                                                                                                                                                       17262 MW;
                                                                                                                                                                                                                                                                                 46.18;
75.08;
                                                                                                                                                                                                                                                                                                                                                  EMBL; D43751; BAA07808.1;
                                                                                                                                                                                                                                                                                                          12; Conservative
                                                                                                                                                                                                                                                                                                                                   10 GKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                        157
157 AA;
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Best Local Similarity
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SEQUENCE
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
VNYPKTLOCAN -> GMHPHRWPEAP (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last nonotation update)
Vitamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                 SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBL_raxID-9615;
                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                     46.5%; Score 65.5; DB 1; Length 277; 60.0%; Pred. No. 0.051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                             CHARGE RELAY SYSTEM (BY S
CHARGE RELAY SYSTEM (BY S
CHARGE RELAY SYSTEM (BY S
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                              BA8A9E8DCFB5D542 CRC64;
                                                                                                   SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 AA.
                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                               InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam: PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        204 AGTK----EGGK-DSCEGDSGGFLV 223
                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGTRYKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                              30570 MW;
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 60.0
Matches 15; Conservative
          ; S01.306; -. HGNC:6361; KLK13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                170
277 AA;
P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                       MIM; 605505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRTC_CANFA
Q28278;
                                                                                                                                                                                              ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                    DISULFID
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                                                                                                                                                                                                                         SITE
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                            Senew;
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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

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09w2c2 drosophila
09w2c4 homo sapien
076520 stomocsphal
078x51 ctenocephal
02xy55 ctenocephal
02xy63 ctenocephal
02xy63 xenopus
879953 xenopus
09vx5 drosophila
          09cw97 mus musculu 018783 macropus eu 091674 xenopus lae 09v5x8 drosophila 08sq23 sus scrofa 063109 rattus norv 09ttr0 canis famil
                                                                                                                                                                                                                                                                                                                 028511 macaca mula
09xy59 ctenocephal
09nbc9 glossina mo
09v1f5 drosophila
045029 drosophila
                                                                                                      O54740 mus musculu
Q99132 mus musculu
                                                                                                                                  mus musculu
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                                                                                                                                               rattus norv
                                                                                                                                                                                    bombyx mori
drosophila
                                                                                                                                                                                                                                                                                                       29bk47 luidia foli
29w5u8 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Banfield D.K., MacGillivray R.T.A.;
"Partial characterization of vertebrate prothrombin cDNAs:
Amplification and sequence analysis of the B chain of thrombin from
nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-!- SIMILARIY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
EMBL; M81396; AAAA31477.1;
--- HSSP; P00734; IUVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                088947 n
Q63207 1
Q60546 n
Q9db10 n
Q8wsj2 bc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001314; Chymotrypsin, InterPro; IPR001254; Ser_protease_Try. Pfam; PF00089; trypsin; 1. PR1072; CHYMOTRYPSIN. SROWOOZO; TRYP_SPC; 1. PROSITE; PS00130; TRYPSIN_DOM; 1. PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1. PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1. HYDOOLER; PS00135; TRYPSIN_HIS; UNKNOWN_1. HYDOOLER; Scile protease. NON_TER SCILE 235 AA; 27093 MW; 92FF3E4F93H3
                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                             Q8SQ23
Q63109
Q9TTR0
                                                                                                                                           Q63207
Q60546
Q9DBI0
                                                                                                                                                                                                                                    09XX61
09XX55
027083
P79953
099RX5
098K47
028511
                                                                                                                 Q99L32
O88947
            Q9CW97
O18783
Q91674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                               09W2C2
08WZB4
076520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-LIVER;
MEDLINE-92212913; PubMed-1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MPX-2002 (TrEMBLrel. 20, MPX-2004)
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                                                                                                                                           482
161
799
1801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; S01.217; -
                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             028731
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
Q28731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      990387 cynops pyrr
991004 gecko gecko
991001 gallus gall
991218 oncorhynchu
990504 eptatretus
990514 acipenser t
98050 drosophila
990wu2 drosophila
990wd8 bufo japoni
990wd8 musculu
99406 mus musculu
99406 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q28731 oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                       May 12, 2003, 15:32:37; Search time 56.5 Seconds (without alignments) 91.171 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                671580
            GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                      671580 seqs, 206047115 residues
                                                                                                                                          US-09-909-348-5
141
1 AGTRYKPDEGKRGDACEGDSGGPFV 25
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                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
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091004
091001
09PTW7
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099WW2
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                      sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_bacteriap:*
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sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                               SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
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Maximum DB seq length: 200000000
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Match Length DB
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76.6
73.0
73.0
70.2
67.4
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20.64
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92FF3E4F93B360E0 CRC64;

O9va44 drosophila O96rq0 homo sapien

Q9VA44 Q96RQ0

Score

Result No.

1117 108 103 103 103 103 70 70 70 70 69 68 68 68 67 5

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LISSUE-LIVER;
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SEQUENCE
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                                                                                                                                                                                                                                                                     Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                                                                                                                                                                                                                                                                            Banfield D.K., MacGillivray R.T.A.; "Partial characterization of vertebrate prothrombin cDNAs: Amplification and sequence analysis of the B chain of thrombin from
                                                                                                                                                                                                                                                                                                                                                                                                                                     nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gecko gecko (Tokay gecko).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gekko.
NCBI_TaxID-36310;
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   Length 235;
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                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 AA; 27272 MW; 49264DD29A57A41F CRC64;
                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
 Score 117; DB 6;
Pred, No. 1.8e-09;
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                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SMO0020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNRNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
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                                                                           167 YKPEEGKRGDACEGDSGGPFV 187
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 83.0%;
95.2%;
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Best Local Similarity 90.5%;
Matches 19; Conservative
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                                                           5 YKPDEGKRGDACEGDSGGPFV
Query Match 83.0
Best Local Similarity 95.2
Matches 20; Conservative
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                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                           Thrombin (Fragment).
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                                                                                                                                                                                                                                                                                                                    WCBI_TaxID=8330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                 090387;
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Q90387
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Banfield D.K., Irwin D.M., Walz D.A., MacGillivray R.T.; "Brolution of prothrombin: isolation and characterization of the cDNAs encoding chicken and hagfish prothrombin."; J. Mol. Evol. 38:177-187(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombin from
                                                                                     Amplification and sequence analysis of the B chain of thrombin from
                                                                                                          nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
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                           Banfield D.K., MacGillivray R.T.A.;
Partial characterization of vertebrate prothrombin cDNAs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
EMBL; M81391; AAA21619.1; -.
HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 AA; 26933 MW; 122A5C09F6F2276A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.0%; Score 103; DB 13;
81.0%; Pred. No. 2.2e-07;
11ve 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  607 AA
                                                                                                                                                                                                                                                                                                          InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam. PF000099; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPIN.
SWART; SW00020; Tryp_SPC; 1.
PR05TIE; PS0240; TryPSIN_DOM; 1.
PR05TIE; PS00134; TRYPSIN_BS; UNKNOWN_1.
PR05TIE; PS00135; TRYPSIN_SR; 1.
Hydrolase; Serine protease.
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InterPro; IPR002383; GLA_blood.
InterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92212913; PubMed-1557383;
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PubMed-1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 YKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                        EMBL; M61392; AAA49309.1; -. HSSP; P00734; 1B7X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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Gaps
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*Partial Characterization of vertebrate prothrombin cDNAs:

Amplification and sequence analysis of the B chain of thrombin from nine different species.*

Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE TRYPSIN FAMILY.

EMBL; M81398; AAAA49433.1; -.

HSSP: P00744; 187X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncorrynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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                                                                                                                                                                                                                                 Score 103; DB 13; Length 608;
Pred. No. 5.9e-07;
2; Mismatches 2; Indels
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81.0%; Pred. No. 8.7e-07;
ive 2; Mismatches 2; Indels
                                                                                                                                                                                   69392 MW; 11B974B9AEE54EA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 239 AA; 27396 MW; FOF43F9A3205BF38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAX-2002 (TrEMBLrel. 20, Last annotation update)
Thrombin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        090504 PRELIMINARY; PRT; 420 AA.
090504;
01-NOV-1996 (TEMBLIEL) 01, Created)
01-NOV-1996 (TEMBLIEL) 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 AA.
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
HydroLase; Serine protease.
     PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS00021; KRINGLE_1; 2.
PROSITE; PS50240; TRINGLE_2; 2.
PROSITE; PS50240; TRYPEIN_DOM; 1.
PROSITE; PS00134; TRYPEIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPEIN_ESE; 1.
HYGYCOLASE; SEATINE PROCECASE.
SEQUENCE 608 AA; 69392 MW; 11B974B9AEE5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-LIVER;
MEDLINE-92212913; Pubmed-1557383;
                                                                                                                                                                                                                                                                                                                                                         539 YSPEDSKRGDACEGDSGGPFV 559
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                                                                                                                                                                                                                                                                                                                                  5 YKPDEGKRGDACEGDSGGPFV 25
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                                                                                                                                                                                                                                 73.0%;
81.0%;
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Best Local Similarity 81.0°
Matches 17; Conservative
                                                                                                                                                                                                                              Query Match 73.0
Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Q90504
ID Q9050
AC Q9050
DT 01-NO
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"Purification and Characterization of Ostrifo prothrombin.";
Int. J. Blochem. Cell Biol. 32:1151-1159(2000)
Int. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE EMBL; AB028871; BaA89046.1; -.
HSSP; P00734; IUVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Struthio camelus (Ostrich).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 103; DB 13; Length 607;
Pred. No. 5.9e-07;
2; Mismatches 2; Indels (
R InterPro; IPR003966; Prothrombin.
R InterPro; IPR001254; Ser_protease_Try.
R InterPro; IPR001254; VitK_dep_GLA.
Péan; PP00591; Kringle; 2.
R Péan; PP00089; trypsin; 1.
R PRINTS; PR00019; GLABLOOD.
R PRINTS; PR00101; GLABLOOD.
R PRINTS; PR001019; GLABLOOD.
R PRINTS; PR001019; RINIGLE.
R PRINTS; PR001019; RINIGLE.
R PRODON; PR001019; KRINGLE.
R PRODON; PR001019; RR; 2.
R SWART; SW00109; Tryp_SPC; 1.
R SWART; SW00101; Tryp_SPC; 1.
R PROSITE; PS00011; GLU_CARBOXILATION; 1.
R PROSITE; PS00011; GLU_CARBOXILATION; 1.
R PROSITE; PS00013; TRYPSIN_DOM; 1.
R PROSITE; PS0013; TRYPSIN_DOM; 1.
R PROSITE; PS0013; TRYPSIN_DOM; 1.
R PROSITE; PS0013; TRYPSIN_DOM; 1.
R PROSITE; PS00134; TRYPSIN_ERR; 1.
Hydrolase; Seline protease.
D SEQUENCE 607 AA; 69110 MW; 002F3605EA36270F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          608 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001314; Chymotrypsin. InterPro; IPR001314; ClA_blood. InterPro; IPR000181; GLA_blood. InterPro; IPR001254; Ser_protease_Try. InterPro; IPR001294; VitK_dep_GLA. Pfam; PF00594; YitK_dep_GLA. Pfam; PF00051; Kringle; 2. Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20579470; PubMed-11137455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539 YSPEDSKRGDACEGDSGGPFV 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 YKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.0%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERODOM; PD000395; Kringle; 2. SWART; SM00069; GLA; 1. SWART; SM00130; FR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 81.0 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prothrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9PTW7
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Bayne C.J., Gerwick L., Fujlki K., Nakao M., Yano T.;
"Immue-relevant (including acute phase) genes identified in the
livers of rainbow trout, Oncorhynchus mykiss, by means of suppression
subtractive hybridization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Partial characterization of vertebrate prothrombin cDNAs: Amplification and sequence analysis of the B chain of thrombin from nine different species.";
                                                                                                                                                                       Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; AF381359; AAG30034.1; --
HSSP; P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acipenser transmontanus (White sturgeon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Chondrostei, Acipenseriformes, Acipenseridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 88; DB 13; Length 172;
Pred. No. 2.6e-05;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 AA; 19873 MW; EC741FBA6957A887 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26846 MW; 45C558D6618E0585 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SMO0020; Tryp_SPC; I.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS01134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      minterpro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Banfield D.K., MacGillivray R.T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92212913; PubMed-1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 YKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V Match 62.4%;
Local Similarity 76.2%;
hes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M81399; AAA48514.1; -. HSSP; P00734; 2HNT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         MEROPS; S01.217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-7904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; S01.217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acipenser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THROMBIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                090244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           090244
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      à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Banfield D.K., Irwin D.M., Walz D.A., MacGillivray R.T.; "Evolution of prothrombin: isolation and characterization of the cDNAs encoding chicken and hagfish prothrombin."; Mol. Evol. 38:177-187(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                 Banfield D.K., MacGillivray R.T.;
"Partial characterization of vertebrate prothrombin cDNAs:
amplification and sequence analysis of the B chain of thrombin from
nine different species.",
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
                                                      Eptatretus stoutil (Pacific hagfish).
Eukaryota; Metazoa; Chordata; Craniata; Hyperotret1; Myxiniformes;
Myxinidae; Eptatretinae; Eptatretus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Banfield D.K.;
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oncorhynchus myklss (Rainbow trout) (Salmo gairdneri).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.4%; Score 95; DB 13; Length 42
76.2%; Pred. No. 6.2e-06;
.ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protesse.
SEQUENCE 420 AA; 47888 MW; 64522AA21A57B67A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Thrombin B chain variant 1 (Fragment).
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser_protease_Try
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                            MEDLINE-92212913; PubMed-1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94223694; PubMed-7513365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 YSPEDMKRGDPCEGDSGGPFV 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0722; CHYMOTRYPSIN, PRINTS; PRO0018; KRINGLE. ProDom; PD000395; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 YKPDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M81393; AAA21620.1; -.
HSSP; P00734; IUVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50070; KRINGLE_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 76.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00051; kringle; 1
Pfam; PF00089; trypsin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00130; KR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRYPSIN FAMILY
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                 NCBI_TaxID=7765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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RESULT 8 Q9DFD1

SCCC SEPTIFICATION OF THE PROPERTY OF THE PROP

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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
BA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrace C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferrace C., Ferriera S., Fleischmann W.,
RA Gong F., Gorge T., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heilman T.J., Hernandez J.R., Honck J.,
RA Harris N.L., Harvey D., Heilman T.J., Wel M.-H., Ibegwam C.,
RA Jalai M., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lia Z.,
Liu X., Maltel B. M., Mortosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Mortis J., Noshrefi A.,
RA Menton S.M., Moy M., Murphy B., Murphy L., Muzry D.M., Nelson D.L.,
RA Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Rabia D.C., Siden-Kamos I., Simpson M., Skupski M.P., Smith T.,
Sylue B.C., Siden-Kamos I., Simpson M., Skupski M.P., Smith T.,
RA Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Walliams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Syliskas R., Tector C., Turner R., Venter E., Wang S., Yao Q.A.,
RA Jenny X.T., Zaveri J.S., Zhan M., Zhou X., Zhu X., Smith H.O.,
RH Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zho X., Smith H.O.,
Rh Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zho X., Smith R. Science 287:2185-2195(2000).
C. -- Similaring S.M. Respendence of Drosophila melanogaster.";
Rybsin Farbing T.R., Parker J. S., Leinner T. Rybsin Family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-OVIDECTAL PARS RECTA;
Hiyoshi M., Takamune K., Mita K., Kubo H., Sugimoto Y., Katagiri C.;
"Oviductin, the oviductal protesse that mediates gamete interaction by
affecting the vitelline envelope in Bufo japonicus: Its molecular
cloning and analyses of expression and post-translational
activation.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buío japonicus (Japanese toad).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Bufonidae, Bufo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 70; DB 5; Length 654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72151 MW; EFBDE951C8247949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase: FBgn0030925; CG6361.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_fry.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00020; Tryp_SPc; 1.
SMSSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00135; TRYPSIN_ESE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRYPSIN FAMILY.
EMBL; AE003509; AAF48845.1; -.
HSSP; P20231; 1AAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00722; CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21, oviductin.
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587 DKNQRKDACQGDSGGPLI 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Serine protease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 61.1 les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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2., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chawez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 70; DB 5; Length 378;
Pred. No. 0.028;
4; Mismatches 3; Indels
                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; AY075342; AAL68205.1; -. SEQUENCE 378 AA; 40548 MW; D355D27E0E929ACC CRC64;
                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
     61.9%; Pred. No. 0.00028;
Live 4; Mismatches 4
                                                                                                                                                                                                                                                                     378 AA
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                                                                                                                                                                                                                                                                     PRT;
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                                                                                                              5 YKPDEGKRGDACEGDSGGPFV 25
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Best Local Similarity 61.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-7227;
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                                                                                                                                                                                                                                                                Q8SY50
Q8SY50;
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Q9VWU2
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Gaps ö

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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                     Nakao M., Ohsaka K., Kato Y., Fujiki K., Yano T.;
"Molecular cloning of complement Clr/Cls/MASP2-like serine proteases from the common carp (Cyprinus carpio).";
Immunogenetics 22:255-263(2001).
-I. SIMILARITY: CONTAINS 2 CUB DOMAINS.
-I. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE PRYPSIN FAMILY.

FRYPSIN FAMILY.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams M.D., Cellitker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helf G., Nelson C.X., Miklos G.L.G.
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSO1186; EGF 2; 1.
PROSITE; PSO1187; EGF_C2; 1.
PROSITE; PSO1187; EGF_C3; 1.
PROSITE; PSO1187; TRYPSIN_DOM; 1.
PROSITE; PSO0135; TRYPSIN_SER; 1.
SGF-11ke domain; Glycoprotein; Hydrolase; Hydroxylation; Setine protease.
SEQUENCE 686 AA: 76200 ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update).
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CG11313 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                          InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000436; Sush1_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20196006; PubMed-10731132;
                      PubMed-11220628;
                                                                                                                                                                                                                                           Chymotrypsin.
CUB_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00181; EGF; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00020; TYP_ESPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS01180; CUB; 2.
                                                                                                                                                                                                                        IPR000152; Asx_hydroxyl
                                                                                                                                                                                                                                                                                  EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                          000089; trypsin; 1. PR00722; CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.2%;
75.0%;
                                                                                                                                                                                                                                                                                                       IPR001881; EGF_Ca.
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     ; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00032; CCP;
                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00431; CUB;
Pfam; PF00008; EGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                            PF00089;
                                                                                                                                                                                                                                                                                                                                                                                                         PF00084
                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsui H., Takahashi T.;
"Mus muscullas mRNA for serine protease-like gene spliced variant-1.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB047758; BAB63919-1; -.
                                                                                                                                                                                                                                                                                                       Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Mopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              092406;
01-DEC-2001 (TERBLE1.19, Created)
01-DEC-2001 (TERBLE1.19, Last sequence update)
01-JUN-2002 (TERBLE1.21, Last annotation update)
28-fine protease-like 1.
Mus musculus (Mouse).
Eukaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus.
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                                                                                                                                                                                                                                                              Length 974;
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80.0%; Pred. No. 0.02;
                                                                      Pfam; PF00431; CUB; 2.
Pfam; PF00699; trypsin; 2.
PROSITE; PS0180; CUB; 2.
PROSITE; PS00140; TRYPSIN_DOM; 2.
PROSITE; PS00134; TRYPSIN_LOM; 2.
PROSITE; PS00135; TRYPSIN_LSER; UNKNOWN_1.
Hydrolase; Seline profease.
SEQUENCE 974 AA; 107647 MW; F19705A470465553 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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Pfam; PF00089; trypsin; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
PHYDROLASE; Protease; Serine protease.
SEQUENCE 200 AA; 22135 MW; 972959E4686EF603 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                         Score 70; DB 13
Pred. No. 0.076;
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                               InterPro; IPR000859; CUB_domain.
InterPro; IPR001254; Ser_protease_Try.
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01-MAR-2001 (TrEMBLrel. 16, C;
01-MAR-2001 (TrEMBLrel. 16, Ls
01-JUN-2002 (TrEMBLrel. 21, Ls
Clrs-A protein.
                                                                                                                                                                                                                                                                                                                                                               227 PEGGK--DACQGDSGGPFL 243
EMBL; AB070367; BAB63372.1;
                                                                                                                                                                                                                                                                                                                                        7 PDEGKRGDACEGDSGGPFV 25
                                                                                                                                                                                                                                                                                                   13; Conservative
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nes 12; Conservative
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NCBI_TaxID=7962;
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Best Local Similarity
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SEQUENCE FROM N.A.
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RESULT 13
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RESULT 14
090602
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Gaps

Ouery Match 47.9%; Score 67.5; DB 5; Length 370; Best Local Similarity 66.7%; Pred. No. 0.065; Matches 12; Conservative 4; Mismatches 1; Indels 1; G

9 EGK-RGDACEGDSGGPFV 25

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Db 309 EGRSRGDSCDGDSGGPLM 326

Search completed: May 12, 2003, 15:38:46 Job time : 57.5 secs

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Novel tripeptide i
Calpain inhibitor.
ACE inhibitor pept
IGF-1 analogue N·t
Angiotensin conver
ACE inhibiting tri
Microbial emetic t
Apolipoprotein A-I
Apolipoprotein A-I
                                                                                        HIV protease inhib
Novel tripeptide 1
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VTL-peptide capabl
Peptide for diagno
                               Chromophore-contg.
Elastase inhibitor
Elastase inhibitor
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Non-RGD, non-YISGR
Potential cross-li
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Peptide AII(1-3) u
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HIV protease inhib
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERA binding domain polypeptide SEQ ID NO 159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                            AAR38408
AAR38409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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WO200153458-A2.
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AAG99717
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New antihypertensi
Hypotensive oligop
Elastase-inhibitin
Cathepsin G inhibi
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ERA binding domain
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New antihypertensi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antihypertensi
                                                                                              May 12, 2003, 15:31:22 ; Search time 2.86 Seconds (without alignments) 46:591 Million cell updates/sec
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/SIDS2/gcddata/geneseq/geneseqp-emb1/AA1981.DAT:*
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                                                                                                                                                                                                                                                                                              908470
             GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                               908470 seqs, 133250620 residues
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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    protein search,

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15-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to ERA binding domain polypeptides ARG99559-ARG99998 and AAM00010-AAM00021). The era gene in Escherichia coli codes for an essential GFPase protein able to autophosphorylate at serine and/or threonine residues. The protein has potential antimicrobial and antibacterial activity and is useful in screening for antagonists, and for compounds with antibiotic activity. The proteins are also useful in determining their role in pathogenesis of infection, dysfunction and disease and could be used as part of a vaccine and/or
                                                       (AAG95559-AAG99999 and AAM00010-AAM00021). The era gene in Escherichia coli codes for an essential Grease protein able to autophosphorylate at serine and/or incenine residues. The protein has potential antimicrobial and antibacterial activity and is useful in screening for antagonists, agonists and for compounds with antibiotic activity. The proteins are also useful in determining their role in pathogenesis of infection, dysfunction and disease and could be used as part of a vaccine and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New ERA binding domain polypeptides and polynucleotides encoding them, useful as research reagents and materials for discovery of treatments and diagnostics for diseases, or for genetic immunisation -
                                                                                                                                                                                                                Gaps
                                              relates to ERA binding domain polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                 ERA binding domain; Escherichia coli; GTPase; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial; antiblotic; pathogenesis; infection; vaccine;
and diagnostics for diseases, or for genetic immunisation
                                                                                                                                                                                         Length 2;
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100.0%; Pred. No. 7.2e+05;
ive 0; Mismatches 0;
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                       Claim 1; Page 26; 279pp; English.
                                                                                                                                                                                                                                                                                                                      AAG99741 standard; Peptide; 2 AA
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                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                               present invention
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Best Local Similarity
Matches 1; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (II) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3.50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
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                                                               Gaps
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Modifying and attaching therapeutic peptides to albumin prevents
reduces the action of peptidases to increase length of activity (
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   Length 2;
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DB 22; L
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100.0%; Pred. No. 7.2e+05;
tive 0; Mismatches 0;
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                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis related peptide SEQ ID NO:1064.
   Score 4;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 543; 733pp; English
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                                                                                                                                                                                                                                                                                                                                        AAB91888 standard; Peptide; 2 AA.
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100.0%;
llarity 100.0%;
Conservative 0;
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99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-112059/12.
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capsules, granules, powder, syrup, suspension, suppositories, ointment, cream, gel, plaster, inhalation compsn. or injection at a dose of 0.001-1000, pref. 0.01-10, mg, 1-3 times per day.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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100.0%; Pred. No. 7.2e+05;
Live 0; Mismatches 0;
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100.0%; Pred. No. 7.2e+05;
ive 0; Mismatches 0;
                                                                                                           New antihypertensive peptide(s) - used to inhibit angiotensin-converting enzyme
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                          (AJIN ) AJINOMOTO KK.
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                                                                WPI; 1989-136272/18.
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                                                                                                                                                                              ; ; 20pp; Japanese.
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Matches 1; Conserv
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Matches 1; Conserv
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7.2e+05;
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:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          Peptides may be derived from extract of fig, and are hypotensive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cathepsin G; elastase; connective tissue; degradation; protease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ë
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by
                                                                                                                                                                         New oligopeptide hypotensive drug - based on alanine, valine, asparagine, proline, isoleucine and arginine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h Similarity 100.0%; Score 4; DB 12; Length 3; Similarity 100.0%; Pred. No. 7.2e+05; 1; Conservative 0; Mismatches 0; Indels
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adult respiratory distress syndrome; para-phenylene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Janusz MJ,
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Peet NP;
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                                                                                                                                                                                                                                                                                    Claim 1; Page 843; 9pp; Japanese.
(AGEN ) AGENCY OF IND SCI TECH. (SHOS ) SHOWA SANGYO KK.
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Modified-site
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       A A X R X P P X S X S S X S S X S S X S S X S S X S S X S S X S S X S S X S S X S S X S S X S S X S S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The peptide and its salts inhibit angiotensin-converting enzyme (ACE) and are useful as antihypertensives. They may be administered orally, parenterally or rectally in the form of tablets, capsules, granules, powder, syrup, suspension, suppositories, ointment, cream, gel, plaster, inhalation compsn. or injection at a dose of 0.001-1000, pref. 0.01-10, mg, 1-3 times per day.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antihypertensive peptide; angiotensin-converting enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 4; DB 10; I
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 1; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antihypertensive peptide(s) - used to inhibit angiotensin-converting enzyme
                                                                                                                                                                         AAP90678 standard; protein; 3 AA.
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                                                                                                                                                                                                                                                                                                                                                                                       New antihypertensive peptide
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AAR10543 RESULT

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WPI; 1993-021449/03.
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Best Local Similarity
Matches 1; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibitors of cathepsin G and elastase for preventing connective tissue degradation are chemically linked inhibitors of the proteases elastase (AAR29095) and cathepsin G (AAR29096).

The N terminal amino acids of the peptides of AAR29095-96 are linked by -C(O)-paraphenylene-C(O)-rape and anti-inflammatory effect useful in the treatment of gout, rheumatoid arthritis and other inflammatory diseases and to prevent elastin mediated tissue damage. It can also be used in the treatment of emphysema and adult respiratory distress syndrome.
The N-terminal amino acids of the peptides of AAR29095-96 are linked by -C(0) paraphenylene-C(0). The cpd has an anti-inflammatory effect useful in the treatment of gout, rheumatoid arthritis and other inflammatory diseases and to prevent elastin mediated tissue damage. It can also be used in the treatment of emphysema and adult respiratory distress syndrome.
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                             Cathepsin G; elastase; connective tissue; degradation; protease; gout; rheumatoid arthritis; emphysema; ARDS; adult respiratory distress syndrome; para-phenylene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide derivs. used as cathepsin G and elastase inhibitors for treating gout, rheumatoid arthritis, inflammatory disorders, emphysema and adult respiratory distress syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "C-terminal Phe is in keto form, i.e. OH replaced by CF3"
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                                                                                                                                                                                                                                                                                                                                                                                                                           the peptides
                                                                                                      100.0%; Score 4; DB 13; Length 3; 100.0%; Pred. No. 7.2e+05; rive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angelastro MR, Bey P, Doherty NS,
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                   AAR29096 standard; peptide; 3 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Page 53; 53pp; English.
                                                                                                                                                                                                                                                                                                       Cathepsin G inhibiting fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RICH ) MERRELL DOW PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                 Sequence
                                                                                                                                                                                                                                                        AAR29096;
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AAR29096
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                                      Gaps
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   Length 3;
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100.0%; Pred. No. 7.2e+05;
ive 0; Mismatches 0;
   DB 13; I
7.2e+05;
 Score 4; DB :
Pred. No. 7.26
); Mismatches
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                                                                                                                                                                                                                                                                                                Metal trapping peptide intermediate.
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                       AAR34022 standard; peptide; 3 AA.
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100.0%; Sc
100.0%; Pr
:ive 0;
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                                                                                                                                                                                                                                                              (first entry)
                                  Conservative
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AAR34023
ID AAR340
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/label- N6-(2-carboxybenzoyl)lysine
/note- "Linked via a linking chain such as
-CO-phenylene-CO- to the N-terminal of a
Cathepsin G inhibiting molecule as described
                                                                                                                                                                                                                                                                                                                                                             The opd. is used for determining interleukin-lbeta convertase (ICE) activity. ICE has been implicated in inflammatory and immune-based diseases including diseases of the lungs and airways, CNS, eyes, ears, joints, bones and connective tissues, cardiovascular system (including the pericardium), GI and urogenital systems and skin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "May opt. be modified by COCOR, CF2CF3, CF3, CHF2, COOR3, CONRR3, CF2CRR3CONRR, H, alkyl, aryl, aralkyl or COR; where R3 is H, alkyl, phenyl or benzyl and R is OH or alkoxy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inflammatory disease; prevention; rheumatoid arthritis; emphysema; neutrophil-mediated connective tissue degradation; gout; elastase; inhibition; adult respiratory distress syndrome.
                                                                                                                                                                                           Maccoss M, Mumford RA, Thornberry NA;
                                                                                                                                                                                                                                                                     New chromophore-contg. cpds. for determining interleukin-lbeta convertase activity in diagnosis of inflammatory or immune-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 4; DB 14; L
100.0%; Pred. No. 7.2e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                   Claim 9; Page 42; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elastase inhibitor peptide #2.
                                                                                                           91US-0746455.
                                                                                92EP-0202450
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/note-
                                                                                                                                                            (MERI ) MERCK & CO INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             mucosal membranes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AA;
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Modified-site
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                                                                                                                                                                                        Chapman KT,
Weldner JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-0CT-1993
                                                                                08-AUG-1992;
                                                                                                           16-AUG-1991;
17-DEC-1991;
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                                                 24-FEB-1993
                   EP528487-A.
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                                                                                                                                                                                                                                                                                                    disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The acyclic peptide (see AAR31340) with metal trapping activity may produced by fragment condensation using the peptide fragments given AAR34022-29.
                                                                                                                                                                                                                                   /note= "Cys(Acm); Acm= acetamidomethyl-protected SH of cystelne"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "alaninyl 7-amino-4-methylcoumarin amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New acyclic peptide with metal trapping activity - exhibits in vivo metal transporting action and can be used as drug, diagnostic agent or functional material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromophore-contg. cpd. for determining ICE activity (3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                           Electrostatic interaction; metalloprotein; binding site; protecting group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-1beta; IL-1b; inflammation; immune; disease; diagnosis; 7-amino-4-methylcoumarin amide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 14; L4
7.2e+05;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "N-acetyl-tyrosinyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 4; DB 100.0%; Pred. No. 7.2 ive 0; Mismatches
                                                                                                                                                                                                                                                                                /note- "OMe protected"
                                                              Metal trapping peptide intermediate.
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                     'note= "HCl.H-Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                          X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 2; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (ICHI-) ICHIKAWA GOSEI KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                             91JP-0120196
                                                                                                                                                                                                                                                                                                                                                                            91JP-0120196
                                (first entry)
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Best Local Similarity
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                               19-MAY-1993
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                                                                                                                                       Synthetic.
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AAR34023;
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AAR3462

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"Linked via a linking chain such as -CO-phenylene-CO- to the N-terminal of a Cathepsin G inhibiting molecule as described in AAR38410-11"
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                                                                                                                                                                                                                                                                                               sequences given in AAR38407-09 are elastase inhibiting peptides
                                                                                                                                                                                                                                                                                                                 which were produced by standard peptide synthesis methods. In the context of the invention they are linked via their N-termini to a Cathepsin G inhibiting peptide (see features table). The peptide conjugates may be used to prevent neutrophil-mediated connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inflammatory disease; prevention; rheumatoid arthritis; emphysema; neutrophil-mediated connective tissue degradation; gout; elastase; inhibition; adult respiratory distress syndrome.
                                                                                                                                                                                                                                                                                                                                                                                      tissue degradation associated with inflammatory diseases eg. gout and rheumatoid arthritis. They may also be used for preventing elastin-mediated tissue damage in the treatment of emphysema and
                                                                                                                                                                                                            cathepsin G and elastase inhibitors - prevents connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14; Length 3; 7.2e+05;
                                                                                                                         Janusz MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 4; DB
100.0%; Pred. No. 7.2
ive 0; Mismatches
                                                                                                                       Doherty NS,
                                                                                                                                                                                                                                                                                                                                                                                                                                             adult respiratory distress syndrome
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                                                                                                                                                                                                                                                                  Claim 9-12; Page 51; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR38409 standard; Protein; 3 AA
                                                                                    (RICH ) MERRELL DOW PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elastase inhibitor peptide #3.
                                                   91US-0704499
                  92ZA-0003602
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Best Local Similarity 100.
Matches 1; Conservative
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                                                                                                                                                                                                                               tissue degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AA;
                                                                                                                     Angelastro MM,
Peet NP;
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                18-MAY-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                   New cathepsin G and elastase inhibitors - prevents connective
                                             Mehd1 S;
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7.2e+05;
                                           Doherty NS, Janusz MJ,
                                                                                                                                                                                                                                                                                                                                                                              Score 4; DB 1
Pred. No. 7.26
; Mismatches
                                                                                                                                                                                                                                                                                                                   adult respiratory distress syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                completed: May 12, 2003, 15:36:05
                                                                                                                                                               Claim 9-12; Page 51; 55pp; English
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                                                                                                                                                                                                                                                                                                                                                                           100.0%;
100.0%;
              (RICH ) MERRELL DOW PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                           Bey P,
                                                                                    WPI; 1993-197380/24
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Best Local Similarity
Matches 1; Conserv
                                                                                                                                   tissue degradation
                                                                                                                                                                                                                                                                                                                                                3 AA;
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Peet NP;
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Job time
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Appl: Appl:

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| Sequence 9, Application US/08122510
| Sequence 9, Application US/08122510
| Patent No. 5464821
| GENERAL INFORMATION:
| APPLICANT: ASSUTU-OLSEN, Stig
| APPLICANT: GAURI, Kallash
| TITLE OF INVENTION: Small peptidic compounds useful for the
| TITLE OF INVENTION: Small peptidic compounds useful for the
| TITLE OF INVENTION: Leatment of Glaucoma
| NUMBER OF SEQUENCES: 14
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Allegretti & Witcoff, Ltd.
| STREET: 10 S. Wacker Dr.
| CITY: Chicago
                                                                                                                                                                                                    Sequence Sequence Sequence Sequence
          sednence
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                         US-08-321-585A-1
US-08-327-392-5
US-08-334-020-36
US-08-338-282-11
US-08-29-150A-38
US-08-29-150A-38
US-08-408-604A-164
US-08-408-604A-164
US-08-408-858A-14
US-08-408-858A-14
US-08-408-858A-14
US-08-408-858A-14
US-08-408-858A-14
                                                                                                                                                                                                                 US-08-451-822A-18
US-08-388-653-40
                                                                                                                                                                                                                                                08-473-985-40
                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0532/91 .
FILING DATE: 25-MAR:1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00095
FILING DATE: 25-MAR:1992
ATTOWNEY/AGENT INFORMATION:
NAME: IWANTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/122,510
FILING DATE: 24-SEP-1993
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Iwanicki, John P
REGISTRATION NUMBER: 34,628
REFRENCE/DOCKET NUMBER: 93,8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34,628
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide FEATURE: NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                               // Search time 0.96 Seconds
(without alignments)
30.649 Million cell updates/sec
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Sequence 14,
Sequence 5, A
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Sequence 30,
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Sequence 13,
Sequence 11,
Sequence 6,
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Sequence 8
Sequence 3
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
             GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08 127-914-5
US-08 603-737-18
US-09-264-709A-29
US-09-264-709A-30
PCT-US94-10475-5
US-07-729-099-5
US-07-729-099-5
US-07-947-035-3
US-07-947-035-3
US-07-947-035-3
US-08-344-618-1
US-08-122-510-3
US-08-122-510-3
US-08-122-510-3
US-08-122-510-3
US-08-122-510-3
US-08-122-510-1
US-08-122-510-1
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-08-213-897A-9
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                                                                                                                                                                                                                                                                                                                                                                               Maximum Match 100%
Listing first 45 summaries
                                                                       protein search, using sw model
                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                               May 12, 2003, 15:33:37
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                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
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                                                                                                                                                         US-09-909-348-4
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CORRESPONDENCE ADDRESS: ADDRESSE: ALGEGRETIE OF WACKER DI. STREET: 10 S. Wacker Dr. CILCAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATER: PATEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.25
CHRRENT APPLICATION DATA:
APPLICATION UMBER: US/08/122,510
FILING DATE: 24-SEP-1993
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COTHER INFORMATION: /note= "Boc-Gly Val-Obzl"
US-08-122-510-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 24-SEP-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0532/91
FILING DATE: 25-MAR-1991
APPLICATION NUMBER: PCT/DK92/00095
FILING DATE: 25-MAR-1992
ATTORRETAMENT INFORMATION:
NAME: IVANICAL, JOHN P
REGISTRATION NUMBER: 34,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93,848
                                                                                                                                                                           Sequence 14, Application US/08122510
Patent No. 5464821
GENERAL INFORMATION:
APPLICANT: AASMUL-OLSEN, Stig
APPLICANT: WIDMER, Fred
APPLICANT: GAURI, Kailash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-08-127-904-5
; Sequence 5, Application US/08127904
; Beten No. 5470951
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 93,8 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000 TELEX: 910/221-5317 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 60606
                                                                                                                                                          US-08-122-510-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: AASMUL-OLSEN, Stig
APPLICANT: WIDMER, Fred
APPLICANT: GAUFI, Kailash
TITLE OF INVENTION: Small peptidic compounds useful for the
TITLE OF INVENTION: treatment of Glaucoma
CORRESPONDENCE ADDRESS:
                                                                                                                                    100.0%; Score 4; DB 1; Length 2; 100.0%; Pred. No. 1.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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. LOCATION: 1..2
; OTHER INFORMATION: /note= "Where X is Benzylester;
; OTHER INFORMATION:
; OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIDATER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,510
FILING DATE: 24-SEP 1993
FILING DATE: 25-MAR-1991
PRIOR APPLICATION NUMBER: DCT/DK92/00095
FILING DATE: 25-MAR-1992
ATFORNEY/AGENT INPOMBATION:
NAME: INAMILER: JOHN PRESERRENCE/POCKET NUMBER: 34,628
REGISTRATION NUMBER: 34,628
RESERRENCE/POCKET NUMBER: 93,848
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Where X is Benzylester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 4; DB 1; IA
illarity 100.0%; Pred. No. 1.7e+05;
Conservative 0; Mismatches
                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Allegretti & Witcoff, Ltd. 10 S. Wacker Dr.
                                                                                                                                                                                                                                                                                                                                  US-08-122-510-10; Sequence 10, Application US/08122510; Sequence 10, Application US/08122510; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 312-715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 520UENCE CHARACTERISTICS: LENGTH: 2 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1.2
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                               Query Match
Best Local Similarity
Lhaq 1; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Sequence 29, Application US/09264709A

Patent No. 6320024

GENERAL INFORMATION

TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and

TITLE OF INVENTION: Improve the Quality of Life

FILE REFERENCE: 2124-310

CURRENT APPLICATION NUMBER: US/09/264,709A

CURRENT APPLICATION NUMBER: 08/79/782

PRIOR FILING DATE: 1999-03-09

PRIOR FILING DATE: 1997-02-07

NUMBER OF SEQ ID NOS: 39

SSOFWARE: Patentin Ver. 2.1

LENGTH: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 4; DB 2; Length 2; 100.0%; Pred. No. 1.7e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 4; DB 4; Length 2; llarity 100.0%; Pred. No. 1.7e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:
COTHER INFORMATION: memory-modulating peptide
US-09-264-709A-29
                                                                                                                           39,911
R: 2026-4186
                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABEL A. BOGGSIAN
REFERENCE/DOCKET NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 2026
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Xaa
OTHER INFORMATION: pher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Conservative
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DESCRIPTION: peptide HYPOTHETICAL: NO
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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OTHER INFORMATION:
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Matches 1; Conserva
                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
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Fatent No. 5849691
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: of Cathepsin D and Plasmepsins I and II
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ő
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                                                                                                                                                                                                                STATE: California
COUNTRY: United States of America
21P: 91010-0269
COMPUTER READABLE FORM:
MEDIUM TYPE: 3M Double Density 5 1/4" diskette
COMPUTER: Wang PC
COMPUTER: A STEM: MS DOS Version 3.20
SOFTWARE: Microsoft
CURRATIO DATE: 29 September 1993
FILING DATE: 29 September 1993
CLASSTEICATION 1424
PRIOR APPLICATION DATA: NO. 5470951e
                                           Protein and Improving the Quality of Life in Individuals With Alzheimer Disease
                                         Amnestic Effects of Amyloid n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7e+05;
                   Method For Antagonizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Irons, Edward S.
REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: No. 5470951e
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/603,737
FILING DATE: February 20, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                            E: City of Hope
1500 East Duarte Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
ANDITHER: IBM PC COMPATIBLE
PO-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
TELEX: NO. 5470951e
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                 TITLE OF INVENTION: Meth
TITLE OF INVENTION: Amne
TITLE OF INVENTION: Prot
TITLE OF INVENTION: Qual
TITLE OF INVENTION: WITH
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
                                                                                                                                                                                                     CITY: Duarte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY:
US-08-127-904-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DS-08-603-737-18
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/729,099
FILING DATE: 19910712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             red. No. 1.7e+05;
Mismatches 0;
                                                                                                                                                                                                                 red. No. 1.7e+05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Binger, Mary-Helen
APPLICANT: Pasamontes, Luis
TITLE OF INVENTION: Coccidiosis Vaccines
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOffmann-La Roche Inc.
              526-3564 or 783-6030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 4; Best Local Similarity 100.0%; Pred. No. Matches 1; Conservative 0; Mismatci
                                                                                                                                                                                                  100.0%; Score 4; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/07729099
Patent No. 5403581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.
                                                                                                                                                                                                                                   ö
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: ROSeman, Catherine R
REGISTRATION NUMBER: 34,24(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 8
TELECOMMUNICATION INFORMATION
                                                               5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Elmeria tenella
                            TELEX: None
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2
                            (202) 783-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMINO ACID
                                                                                                               Amino Acid
                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 1; Conserv
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                                                                                                                TYPE: Amino
STRANDEDNESS
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              TELEPHONE:
TELEFAX: (
                                                                                                                                                ; TOPOLOGY:
PCT-US94-10475-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 4; DB 4; Length 2; llarity 100.0%; Pred. No. 1.7e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: memory-modulating peptide US-09-264-709A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antagonizing Amnestic
Effects of Amyloid n
Protein and Improving
the Quality of Life
in Individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U. S. Application
Serial No.
08/127,904; filled
29 September 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             With Alzheimer Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
COUNTRY: United States of America
ZIP: 91010-0269
COMPOTER. READABLE FORM:
MEDIUM TYPE: 3M Double Density 5 1/4"
MEDIUM TYPE: 14skette
COMPUTER: Wang PC
COMPUTER: Wang PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MS DOS Version 3.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US94/10475
FILING DATE: 16 September 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application PC/TUS9410475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: City of Hope
1500 East Duarte Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: NO
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: 08, PRIOR APPLICATION DATA: 29 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microsof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Applicat:
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duarte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-US94-10475-5
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Gaps

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APPLICANT: Francis, Geoffrey L.
APPLICANT: Walton, Paul E.
APPLICANT: Walton, Paul E.
APPLICANT: Manuty, John P.
APPLICANT: Phelps, Patricia V.
TITLE OF INVENTION: Method of Administering IGF-1, IGF-2, ITILE OF INVENTION: and Analogs Thereof to Birds
NUMBER OF SEQUENCES: 18
               COMPUTER: IBM PC/386 COMPOTED:
COMPUTER: Word 5.5-t
SOFTWARE: Word 5.5-t
CURRETA APPLICATION DATA:
APPLICATION NUMBER: US/08/118,135A
FILING DATE: September 8, 1993
CLASSIETCATION ATA:
APPLICATION DATA: NO. 5437982e
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: UOFW16993
TELECHOWN: 1-206-682-8100; 1-206-224-0709 (direct)
TELECHOME: 1-206-682-8100; 1-206-224-0709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: BAPLICATION DATE: 17-SEP-1992 CLASSIFICATION: 514 CLASSIFICATION: 514 CLASSIFICATION: 514 CLASSIFICATION: 31,665
Diskette-5.25 inch, 1.2Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 4; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 1; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide DESCRIPTION: page 22, line 17; VFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 28234
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Kenneth D. Sibley
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 5444045th Carolina
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/07947035 Patent No. 5444045
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(919) 881-3175
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 4938023
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-118-135A-8
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Patent No. 5437982
GENERAL INFORMATION:
APPLICANT: Catterall, W.A. and Eaholtz, G.
TITLE OF INVENTION: "Specific Inactivation Gate Inhibitors of the Sodium Channel"
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
                                                                                                                                                                                                                                      INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TREATING USING THE SAME
                                                                                                                                                                                                                  POLYPEPTIDE, DNA FRAGMENT ENCODING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3;
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Burns, Doane, Swecker & Mathis ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: Z2313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
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illarity 100.0%; Pred. No. 1.7e+0;
Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET UNBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
                                                               Sequence 38, Application US/07791213D Patent No. 5409895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                      APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, TOSHINOFI
APPLICANT: NOBUHARA, MASAHITO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        TITLE OF INVENTION: POLY
TITLE OF INVENTION: SAME
TITLE OF INVENTION: TREA
TITLE OF INVENTION: TREA
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-07-791-213D-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
GY: linear
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Best Local Similarity
Matches 1; Conserva
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                                                                                                                  GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: SUZUKI, Nacyoshi
TITLE OF INVENTION: A No. 5464819el Physiologically Active Peptide Having
TITLE OF INVENTION: Immunoregulatory Activities
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BURTON, James
APPLICANT: DONG, Zhengarin
APPLICANT: PRIGO, Timothy B.
TITLE OF INVENTION: SPECIFIC INHIBITORS OF TISSUE KALLIKREIN
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 555 13th Street, N.W., Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 4; DB 1; Length 3; 100.0%; Pred. No. 1.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                            CITY: Falls curstrains STATE: Virginia COUNTRY: United States of America ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/729,353 FILING DATE: 19910712 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 139, Application US/08079812
Patent No. 5464820
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOLDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-182714
FILING DATE: 12-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                               Sequence 6, Application US/07729353
Patent No. 5464819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Svensson, Leonard R. REGISTRATION NUMBER: 30,330 REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YELECOMMUNICATION INFORMATION TELEPHONE: 703 241 1300 TELEFRAX: 703 532 3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-07-729-353-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 1/
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CITY: Wa
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nakamura, Yasunori
APPLICANT: Takano, Toshiaki
TITLE OF INVENTION: Angiotensin Convertin Enzyme Inhibitor
TITLE OF INVENTION: and Method for Preparing Same
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby
STREET: 805 Third Ave.
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3;
                                                                                                                                                                            Length 3;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 4; DB 1; IA
illarity 100.0%; Pred. No. 1.7e+05;
Conservative 0; Mismath
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/090,530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 4/197239
FILING DATE: 23-JUL-1993
ATTORNEY AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 4703/08
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08384618
Patent No. 5449661
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-7513
                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEK. 236687
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 Conservative
SEQUENCE CHARACTERISTICS LENGTH: 3 amino acids
                                                                                           : peptide
NO
                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
Matches 1; Conserva
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                                                                           linear
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Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 805 Th1
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino a STRANDEDNESS:
                                                                           TOPOLOGY: 11:

MOLECULE TYPE:

HYPOTHETICAL: 1

US-07-947-035-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE:
US-08-384-618-1
                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-08-384-618-1
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Washington

STATE:

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COMPUTER READABLE FORM:

MUDIUM TYPE: RIOPY disk

MUDIUM TYPE: RIOPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/079,812

FILING DATE: 22-JUN-1993

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Rememble, James

REFERENCE/COCKET NUMBER: 16865-0118

TELECOMUNICATION INFORMATION:

TELECOMUNICATION NUMBER: 1685-0118

TELECOMUNICATION NOT 139:

TELEPHONE: (202) 639-7832

INFORMATION FOR EQUID NO: 139:

SEQUENCE CHARACTERISTICS:

LENGTH: 3 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: maino acids

TYPE: maino acids

TYPE: maino acids

TYPE: TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: MODIfied-site

LOCATION: 3

US-08-079-812-139

QUELY MATCH

LOCATION: 3

US-08-079-812-139

QUELY MATCHES 1; Conservative 0; Mismatches 0; Indels 0; Gaps
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Search completed: May 12, 2003, 15:40:40 Job time: 1.96 secs

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May 12, 2003, 15:38:52; Search time 1.94 Seconds (without alignments) 47.436 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                    349150 seqs, 92025710 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                Sequence:
                                                                                                                               Run on:
                                                                                                                                                                                                                   Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US10_PUBCOB.pep:*/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

/prodata/1/pubpaa/PCTUS_PUBCOMB.pep:*/ptcdata/1/pubpaa/US08_PUBCOMB.pep:*/ptcdata/1/pubpaa/US09_NEW_PUB.pep:*

ptodata/1/pubpaa/US09_PUBCOMB.pep

/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:* /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

/cgn2_6/ptodata/1/pubpaa/US07_

Result Query No. Score Match Length DB ID 1 4 100.0 2 10 US-09-982-172-152 2 4 100.0 2 10 US-09-982-172-152 3 4 100.0 3 10 US-09-982-172-152 5 4 100.0 3 9 US-09-982-172-152 5 5 6 4 100.0 3 9 US-09-982-173-11 5 6 4 100.0 3 9 US-10-015-979-11 5 7 4 100.0 3 9 US-10-015-979-11 5 8 4 100.0 3 10 US-09-982-11 5 8 4 100.0 3 10 US-09-983-91 5 8 4 100.0 3 10 US-09-983-91 5 8 6 100.0 3 10 US-09-813-81 5 8 6 100.0 3 10 US-09-813-81 5 8 100.0 3 10 US-09-813

APPLICANT: Entl Israel Katz
TITLE OF INVENTION: PRETIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBO
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENE
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172

Sequence 19, Appl Sequence 10, Appl Sequence 25, Appl Sequence 47, Appl Sequence 84, Appl Sequence 11, Appl Sequence 12, Appl Sequence 17, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 52, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 56, Appl Sequence 57, Appl		POLYPEPTIDES OF INTEREST AND ANTIBO METHODS, SYSTEMS AND KITS FOR GENE C peptide C peptide C beptide C Length 2; C Length 3; C Length 4; C Length 5; C Length 6; C Length 6; C Length 7; C	
3 10 US-09-972-475-19 3 10 US-09-895-443-10 3 10 US-09-984-056-25 3 10 US-09-984-172-47 3 10 US-09-982-172-84 3 10 US-09-983-172-84 3 10 US-09-983-172-84 3 10 US-09-983-629-17 4 8 US-08-839-248-3 4 8 US-08-845-92-4 8 US-08-842-92 4 8 US-08-987-689A-15 4 8 US-08-881-219-10 5 US-08-884-409-5 6 US-08-484-409-19	ALIGNMENTS	US/09982172 tz EES REPRESENTATIVE OF CTED THEREAGAINST, AND IZING EACH R: US/09/982,172 1-10-19 n 3.1 n 3.1 uence ter generated syntheti ter generated syntheti er generated syntheti ter generated syntheti 0.0%; Score 4; DB 10 0.0%; Pred. No. 3e+05 e 0; Mismatches	nn US/09982172 Nai
20 21 22 23 24 25 25 26 27 27 28 29 20 20 20 20 20 20 20 20 20 20	:.	**SEULT 1 **Sequence 145. Application US/09982172 **Sequence 145. Application US/09982172 **Sequence 145. Application US/09982172 **Sequence 145. Application US/09982172 **Septence INVENTION: PEPTIDES REPRESENTATIVE **TITLE OF INVENTION: DIRECTED THEREAGAINST, **TITLE OF INVENTION: UTILIZING EACH **TITLE OF INVENTION: UTILIZING EACH **TITLE OF INVENTION: UTILIZING EACH **SET OF RED INVENTION: UTILIZING EACH **SEQ ID NOS: 253 **SEPTION: SEQ ID NOS: 253 **SEQ ID NOS: 253 **SEQ ID NO 145 **SEQ ID NO 145 **TYPE: PRT **OFTHANE: PRT **OFTHANE: Artificial sequence **FEATURE: **OTHER INFORMATION: Computer generated syntl US-09-982-172-145 **QUETY MATCH **Best Local Similarity 100.0%; Score 4; DI **Best Local Similarity 100.0%; Pred: No. 36 **Matches 1; Conservative 0; Mismatchee	Db 1 V 1 RESULT 2 US-09-982-172-152 ; Sequence 152, Application US; Patent No. US20020137119A1 ; GENERAL INFORMATION:

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APPLICANT: White, Frost
APPLICANT: White, Frost
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: Alzheimer's Disease
TITLE OF INVENTION: Alzheimer's Disease
TITLE OF INVENTION: Alzheimer's Disease
CURRENT APPLICATION NUMBER: US/9/9/826,290
CURRENT APPLICATION NUMBER: 2001-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/09900936
Patent No. US20020165141A1
Patent No. US20020165141A1
APPLICANT: Nodgers, Kathleen
APPLICANT: dizerega, Gere
APPLICANT: dizerega, Gere
TITLE OF INVENTION: Or Differentiation
FILE REFERENCE: 00-506-A
CURRENT APPLICATION NUMBER: US/09/900,936
CURRENT APPLICATION NUMBER: US/09/900,936
CURRENT PILING DATE: 2001-07-09
NUMBER OF SEO ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: Durham, L.Kathryn
APPLICANT: Friedman, David L.
APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 492
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 464
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: US 60/253,647
PRIOR FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/194,504
                                                                                                                                                                                                                                         Application US/09826290
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Rajesh Bhikhu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            llber, B. Michael
tiger, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           David M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: homo sapien US-09-826-290-464
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Best Local Similarity
Matches 1; Conserv
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US-09-900-936-11
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LENGTH: 3
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                                                                                                                                                                                                                                  FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D377/AP6D
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                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 4;
ilarity 100.0%; Pred. No.
Conservative 0; Mismatral
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CACSH M. DESAI

THOMAS P. LEARY

APPLICANT: JAMES C. ERKER

APPLICANT: JAMES C. ERKER

APPLICANT: JAMES C. ERKER

TITLE OF INVENTION: NON-A.

NUMBER OF SEQUENT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: ABBOTT LABORATORIES: 100 ABBOTT PARK ROAD ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOHN N. SIMONS
TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435435
NTTORNEY/AGENT INPORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
SEQ ID NO 152
LENGTH: 2
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Best Local Similarity 100.0%;
Matches 1; Conservative 0;
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ELECOMMUNICATION INFORMATION
TELEPHONE: 708-937-6365
                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 1; Conserv
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ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 186, Applica
Patent No: US20020119
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-424-550B-186
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STREET: 10
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STATE:
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Gaps

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Length 3;

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OTHER INFORMATION: Description of Artificial Sequence: CB4 domain of mutant 18
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                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Motif 4, corresponding to residues 188 to 190 of US-10-039-876A-6
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                              PPLICANT: Blumberg, Hal
ITLE OF INVENTION: A HUMAN 2-19 PROTEIN HOMOLOGUE, 2219A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 4; DB 9;
; Pred. No. 3e+05;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 4; DB 9; 100.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                 CURRENT APPLICATION NUMBER: US/10/039,876A
                                                                                                       CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 60/061,712
PRIOR PILING DATE: 1997-10-06
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Verhaert, Raymond M.D.
APPLICANT: Beekwilder, Martinus J.
APPLICANT: Achle, Wolfgang
TITLE OF INVENTION: Enzyme Selection
FILE REFERENCE: 2183-5207US
CURRENT APPLICATION NUMBER: US/10/015,979
CURRENT FILING DATE: 2001-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 4; 100.0%; Pred. No.
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FILING DATE: 2000-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/138,443
PRIOR FILING DATE: 1999-06-10
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US-10-015-979-71
; Sequence 71, Application US/10015979
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                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin version 3.1
SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                      ILE REFERENCE: 97-63C1
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Best Local Similarity
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Matches 1; Conserv
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: OTHER INFORMATION:

US-10-015-979-63
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NAME/KEY: SITE
                                                                                                                                                                                                                                                         SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: Designed polypeptide with anti-inflammatory, anti-bacterial, anti OTHER INFORMATION: -fungal and antipyretic properties.
US-09-828-272A-1
                          Gaps
                                                                                                                                                                                                                                                                         APPLICANT: LIPTON, James M
APPLICANT: CATANIA, Anna P
TITLE OF INVENTION: USE OF KPV TRIPEPTIDE FOR DERMATOLOGICAL DISORDERS
FILE REFERENCE: 259/058
CURRENT APPLICATION NUMBER: US/09/828,272A
CURRENT FILING DATE: 2001-04-06
NUMBER OF SEO ID NOS: 7
SOFTWARE: Patentin version 3.1
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  Pred. No. 3e+05;
; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
FILE REFERENCE: 08191-022001
CURRENT APPLICATION NUMBER: US/10/074,956
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/268,175
PRIOR FILING DATE: 2001-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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                                                                                                                                                                                                             Sequence 1, Application US/09828272A Publication No. US20020183255A1 GENERAL INFORMATION:
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Publication No. US20020193332A1
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  100.08;
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Best Local Similarity 100.
Matches 1; Conservative
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US-10-074-956-5
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Best Local Similarity
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TITLE OF INVENTION Methods for Inhibiting Smooth Muscle Cell Proliferation 1TILE REFERENCE: 99-1043-A CURRENT APPLICATION NUMBER: US/09/771,192
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 3
THE PATENT FILING DATE: 2.0
SEQ ID NO 11
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; OTHER INFORMATION: Description of Artificial Sequence:AII (1-3)
US-09-771-192-11
                                                   APPLICANT: Chu, Ivan K.
APPLICANT: Lau, Tai-chu
APPLICANT: Lau, Tai-chu
APPLICANT: Lau, Tai-chu
TITLE OF INVENTION: Sequencing of Peptides by Mass Spectrometry
FILE REFERENCE: 7933.208-U3.
CURRENT APPLICATION NUMBER: US/09/804,866
CURRENT FILING DATE: 2001-03-13
PRIOR FILING DATE: 2000-03-13
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
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, Application US/09804866
US20020001814A1
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ORGANISM: Artificial Sequence
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; OTHER INFORMATION: X is Q or
US-09-804-866-14
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Matches 1: Conserv
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US-09-853-918-6
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RPLICANT: Kim E. Leitzel
ITLE OF INVENTION: Sensitive Detection of Wild-Type and
ITLE OF INVENTION: Mantant EGFR by Specific ELISA Assays
ITLE OF INVENTIONS: Sample
                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:
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.3e+05;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 3
                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/015,979
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CURRENT FILING DATE: 2001-03-12
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Pred. No.
                                                                                                                                                                               URRENT FILING DATE: 2001-12-10
FRIOR APPLICATION NUMBER: PCT/NL00/00399
FRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/138,443
                                     APPLICANT: Quax, Wilhelmus J.
APPLICANT: Verhaert, Raymond M.D.
APPLICANT: Beekwilder, Martinus J.
APPLICANT: Aehle, Wolfgang
TITLE OF INVEWIION: Enzyme Selection
FILE REFERENCE: 2183-52070S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/188,424
PRIOR FILING DATE: 2000-03-10
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Patent No. US20010046686A1
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APPLICANT: Albert J. Wong
APPLICANT: David K. Moscatello
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ilarity 100.0%;
Conservative 0
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Conservative 0
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PRIOR APPLICATION NUMBER: 60/13
PRIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin version 3.1
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US20030036050A1
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US-09-803-854-9
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Best Local Similarity
Matches 1; Conserva
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Matches 1; Conserv
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; LOCATION: (1)..(3)
; OTHER INFORMATION:
US-10-015-979-71
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US-09-804-866-14
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RPLICANT: TSERNIGS, Lars
ITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
ILLE REFERENCE: 033315-002
                                                    TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: DEBAUN
CURRENT APPLICATION NUMBER: US/09/853,918
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,448
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 65
SOFFWARE: PATENTIN VEY: 2.0
SEQ ID NO 6
LENGTH: 3
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CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION UNDBER: US 09/095,106
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: PCT/SE96/01621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1996-12-09
PRIOR APPLICATION NUMBER: SE 9504467-3
PRIOR FILING DATE: 1995-12-12
PRIOR APPLICATION NUMBER: GS 60/009,386
PRIOR FILING DATE: 1995-12-29
SEQ ID NOS: 44
SOFTWARE: PATENTIN NOT. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31, Application US/09850061A Patent No. US20020094957A1
Mouravieff, Julie E.
Einspahr, Howard M.
Kish, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NORDSTEDT, Christer
APPLICANT: NASLUND, Jan
APPLICANT: THYBERG, Johan
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milarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-918-6
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; ORGANISM: Amyloidosis
US-09-850-061A-31
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Search completed: May 12, 2003, 15:59:10 Job time : 2.94 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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                                                                               OM protein - protein search, using sw model
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Gapop 10.0., Gapext 0.5
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Maximum DB seq length: 2000000000
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Description	anglotensin-conver	phenol 2-monooxyge	22K superhelical D	cell surface adhes	hypothetical prote	ribosomal protein	glucan 1,4-alpha-g	hypothetical prote	schwannomin - mous	branched-chain-ami	glycogen phosphory	peptidyl-dipeptida	copper resistance	R-phycoerythrin al	anglotensin-conver	hypothetical prote				cocoonase (EC 3.4.	myosin light chain	phosphoprotein, bo	Ig heavy chain CRD	27.5 kda structura			×	uctural pr	alcohol dehydrogen
ID	PO0010	A37832	A61300 .	B43848	146627	S17255	A27897	T30569	I54357	A40135	A60521	JN0862	C41225	B22565	PQ0009	T14908	T14910	S55237	A44692	B61168	I50385	S11127	PT0278	G44817	144817	E44817	C44817	44	S66195
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Query Match
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Matches 1; Conservative 0; Mismatches 0; Indels

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					ALIGN	ALIGNMENTS	
RESULT 1 PQ0010 anglotensin-converting N,Alternate names: fic C,Species: Flcus carior C,Date: 15-Jun-2001 #sc C,Accession: PQ0010 R,Maruyama, S.; Miyosh, Agric: Biol Chem. 53, Agritle: Anglotensin I A,Reference number: PQ0 A,Accession: PQ0010 A,Accession: PQ0010 A,Residues: 1-3 <arara a,experimental="" anglotensii<="" c,keywords:="" source:="" td=""><td>-conversion and a conversion and a conve</td><td>stn-converting enzyme inhimate names: ficus latex peps: Flous carica (common fils-Jun-2001 #sequence_revilon: PQ001 #sequence_revilon: PQ001 #sequence_revilon: PQ001 I-converting for number: PQ0008 for n</td><td>enzyme in s latex j (common quence_r , S.: Ta 2763-276 convertin n n</td><td>at in 178 property of 178 prop</td><td>1bltor (1916) 15 (1916) 15 (1916) 15 enzyme</td><td>(FLP-3) - common fig 15-Jun-2001 #text_change 15-Jun-2001 e inhibitors derived from Ficus carica me inhibitor</td><td></td></arara>	-conversion and a conversion and a conve	stn-converting enzyme inhimate names: ficus latex peps: Flous carica (common fils-Jun-2001 #sequence_revilon: PQ001 #sequence_revilon: PQ001 #sequence_revilon: PQ001 I-converting for number: PQ0008 for n	enzyme in s latex j (common quence_r , S.: Ta 2763-276 convertin n n	at in 178 property of 178 prop	1bltor (1916) 15 (1916) 15 (1916) 15 enzyme	(FLP-3) - common fig 15-Jun-2001 #text_change 15-Jun-2001 e inhibitors derived from Ficus carica me inhibitor	
Query Match Best Local Matches	η S1π 1;	Similarity 100 1; Conservative	100 100 ative	100.0%; 100.0%; Eive (Sc. Pr.	ore 4; DB 3; Length 3; ed. No. 0; Mismatches 0; Indels 0; Gaps	. :0
Oy 1 V Db 2 V	7 7						
RESULT 2 A37832 phenol 2-monooxygenase (EC C; Species: Pseudomonas ap. C; Date: 14-Jun-1991 #sequen C; Accession: A37832 R; Powlowski, J.; Shingler, J. Bacteriol. 172, 6834-684 A; Title: In vitro analysis A; Reference number: A37832, A; Accession: A37832 A; Residues: 1-4 < Pow>C; Keywords: oxidoreductase	nnooxyg Pseudo Jun-19 11. A378 11. 172 11. 172 11. 172 11. 173 11. 173 11. 174 11. 14. 4	2-monooxygenase (EC 1. es: Pseudomonas ap. ald-Jun-1991 #sequence alon: A37832 wski, J.; Shingler, V. eriol. 172, 6834-6840, eriol. 172, 6834-6840, es: In vitro analysis of ence number: A37832; M sion: A37832 ws. preliminary ule type: protein ues: 1-4 <pow></pow>	7 0 200	14.13 Lrevii 1990 Polym	sion sion pept	in P5 - Pseudomonas sp. (strain -Jun-1991 #text_change 23-Jun-19 requirements of multicomponent ; PMID:2254259	CF600) (frag 193 phenol hydro

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Rigrohmann, L.; Graack, H.R.; Kruft, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, FEBS Lett. 284, 51-56, 1991
A;Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit fr A;Reference number: S17255; MUID:91285106; PMID:2060626
                                                                              mitochondrial, questionable - yeast (Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Morrice, J.; MacKenzie, D.A.; Parr, A.J.; Archer, D.B.
Curr. Genet. 34, 379-385, 1998
A;Title: Isolation and characterisation of the acetyl-CoA carboxylase gene from Asper
A;Reference number: 220869; MUID:99087906; PMID:9871120
                                                                                                                                                                                                                                                                                                                                                                           C; Comment: A coding region for this protein could not be identified in the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Inokuchi, N.; Takahashi, T.; Irie, M.
J. Balcohen. 90, 1055-1067, 1981
A;Title: Purification and characterization of a minor glucoamylase from Aspergillus A;Reference number: A27897; MUID:82075730; PMID:6796572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 06-Dec-1996
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C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C;Accession: T30569
                                                                                                                                                     C;Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-May-1997
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C;Keywords: mitochondrion; protein biosynthesis; ribosome
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A; Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 0;
Mismatches
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A; Accession: A27897
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A; Residues: 1-4 <GRO>
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Best Local Similarity
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R; Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
submitted to the EMBL Data Library, July 1995
A; Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do
A; Reference number: 223105
                                                                 C; Accession: A61300

Kishi, F.; Ebina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.
J. Biochem. 92, 1059-1068, 1982.
A; Title: Purification and characterization of a protein from Escherichia coli which form A; Reference number: A61300; MUID:83082696; PMID:6294066
                                                                                                                                                                                                                                              A;Residues: 1-4 <KIS>
C;Comment: This protein resembles some of the histone-like protein of bacteria in amino
C;Reywords: DNA binding; monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            surface adhesin for heparan sulfate, 60K - Staphylococcus aureus (fragment)
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                    s: Escherichia coli
17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
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Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
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perhelical DNA-binding protein - Escherichia coli (fragment)
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A;Cross-references: EMBL:U31309; NID:g974285; PID:g974292
A;Experimental source: strain s6PT2xs6PT3; 8 month seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-4 <LIA>
A;Note: sequence extracted from NCBI backbone (NCBIP:85444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
Nect. Immun. 60, 899-906, 1992
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Best Local Similarity 100.0%;
Matches 1; Conservative 0
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Best Local Similarity 100.0%;
Matches 1; Conservative 0
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pertidy1-dipeptidase A inhibitory peptide C112 - striped bonito
C;Species: Sarda orientalis (striped bonito)
C;Species: Sarda orientalis (striped bonito)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: JN0862
R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Blotechnol. Biochem. 57, 1744, 1993
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory
A;Reference number: JN0859; MUID:94080036; PMID:7764272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: intestine C; Comment: The amino terminal tripeptide of this protein inhibits angiotensin I-conve C; Superfamily: bradykinin-potentiating peptide C; Keywords: anglotensin-converting enzyme inhibitor
     A;Residues: 1-5 <BON>
C;Superfamily: phosphorylase
C;Reywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status expe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer
A;Reference number: A41225; MUID:92020961; PMID:1924351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Pseudomonas syringae pv. tomato
C:Date: 19-1un-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C:Accession: C41225
R:Cha, J.S.; Cooksey, D.A.
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llarity 100.0%; Pred. No.
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A;Molecule type: protein
A;Residues: 1-5 <CHA>
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nes 1; Conserv
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                                                                                                                                                                                                                                                                                                                                                  R; Huynh, D.P.; Nechiporuk, T.; Pulst, S.
Mum. Mol. Genet. 3, 1075-1079, 1994
A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are cd
A;Reference number: I54357; MUID:95072570; PMID:7981675
A;Accession: I54357
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K. Bonamusa, L.; Baanante, I.V.
Comp. Blochem. Physiol. B 95, 295-301, 1990
A; Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
A; Reference number: A60521; MUID:90227907; PMID:2109669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                branched-chain-amino-acid transaminase (EC 2.6.1.42), mitochondrial - rat (fragment)
N/Alternate names: branched-chain-amino-acid aminotransferase, mitochondrial
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                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 02-Aug_1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Rattus norvegicus (Norway rat)
Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 30-Sep-1993
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C'Species: Liza ramada
C'Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
                               Gaps
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A;Cross-references: GB:L28838; NID:g454836; PIDN:AAA57150.1; PID:g601923
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C;Accession: A40135
R;Hutson, S.M.; Wallin, R.; Hall, T.R.
submitted to the Protein Sequence Database, March 1992
A;Reference number: A40135
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A:Molecule type: mRNA
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A Molecule type: protein
A? Residues: 1-4 < HUT>
C; Keywords: aminotransferase; mitochondrion
Best Local Similarity 100.0%; P
Matches 1; Conservative 0;
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A;Molecule type: protein
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Agric. Biol. Chem. 53, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A;Reference number: PQ0008
A;Accession: PQ0009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       angiotensin-converting enzyme inhibitor (FLP-2) - common fig
N;Alternate names: flcus latex peptide 2
C;Species: Flcus carica (common fig)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
C;Accession: PQ0009
A; Title: Characterization of the bilin attachment sites in R-phycoerythrin. A; Reference number: A22565; MUD: 85182601; PMID: 3886644
A; Accession: B22565
A; Accession: B22565
A; Molecule type: protein
A; Residues: 1-5 <KLO>
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A; Residues: 1-5 <MAR>
A; Experimental source: latex
C; Keywords: anglotensin-converting enzyme inhibitor
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Search completed: May 12, 2003, 15:39:44 Job time: 2.14 secs

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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2003, 15:32:07; Search time 0.58 Seconds

(*Athout alignments)

71.511 Million cell updates/sec
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Title: US-09-909-348-4

Perfect score: 4
Sequence: 1 V 1
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	homo sa	sacch	P82099 litoria rub	P82100 litoria rub	P82070 litoria rub	_	P54714 canis famil	P80628 zea mays (m	-	mytilus	P13737 mytilus edu		P20104 enterococcu	achatina	P35920 achatina fu	P35921 achatina fu		-		010582 bothrops ja	-	P80488 thiobacillu	-	-	P81010 fusarium so	P04548 periplaneta	P81152 mycobacteri		P82618 periplaneta		P30096 homo sapten	0 herpes s	P80975 thunnus obe
SOMMALES	QI .	EOSI_HUMAN	RM01_YEAST	EI03_LITRU	EI04_LITRU	RE11_LITRU	RE32_LITRU	TPIS_CANFA	UC22_MAIZE	ACPH_RABIT	CIP1_MYTED	CIP2_MYTED	EI01_LITRU	CCF1_ENTFA	WWA1_ACHFU	WWA2_ACHFU	WWA3_ACHFU	ACT_CARMA	AKHG_GRYBI	AKH_LIBAU	ANG2_BOTJA	CAD1_ENTFA	CLP_THICU	COW2_CONPU	- 1	FUSS_FUSSO	~		PLP_BRANA	PPK3_PERAM	UPA1_HUMAN	UPAA_HUMAN	VGLG_HSV2B	COXE_THUOB
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[1] SEQUENCE. MEDLINE-91285106; PubMed-2060626; Grohmann L., Graack H.-R., Kruft V., Choll T., Goldschmidt-Reisin S.,

S K R R S S

LERYPA P82661 panagrellus P19346 erythrocebu P19346 erythrocebu P80159 treponema h P42996 scyllorhinu P41899 scyllorhinu P42998 eisenia foe P42996 ergenia foe P43000 gqualus aca P81179 diaprepes a P24047 stomopneute CALVO P41517 calliphora	ALIGNMENTS ed) sequence update) annotation update) a; Craniata; Vertebrata; Euteleostomi; s; Catarrhini; Hominidae; Homo. 60093; of eosinophilotactic tetrapeptides of cation as eosinophil chemotactic factor of A. 72:4123-4127(1975). PTIDES ARE RELEASED FROM MAST CELLS IN LUNG ING HYPRESENSITIVITY RECTING EMOTAXIS; CHEMOTACTIC DEACTIVATION, RELEASE TION OF THE HEXOSE MONOPHOSPHATE SHUNT. V -> A (IN OTHER PEPTIDE). '/FRIG-VAR_005201. 6B05B862A0000000 CRC64; Score 4, DB 1; Length 4;	ed. NO. U; Mismatches 0; Indels 0; Gaps 0; T; 4 AA. T; 4 AA. Tce update) ation update) ein Li (Ymil) (Fragment). syeast). ccharomycctina; Saccharomycetes; aceae; Saccharomyces.
34. 4 100.0 9 1 FARS_PANRE 35 4 100.0 9 1 FIBB_ERYPA 36 4 100.0 9 1 FLAZ_TREHY 37 4 100.0 9 1 LAT3_LOCMI 39 4 100.0 9 1 LAT3_LOCMI 40 4 100.0 9 1 OXYE_SCYCA 41 4 100.0 9 1 OXYE_SCYCA 42 4 100.0 9 1 OXYE_SCYCA 42 4 100.0 9 1 OXYE_SCHOOL 43 4 100.0 9 1 PGLR_DIABA 44 4 100.0 9 1 SAP_STOVA 45 4 100.0 9 1 TRCI_CALVO	RESULT 1 BOST_HUMAN STANDARD; PRT; 4 AA. AD EDSILHUMAN STANDARD; PRT; 4 AA. DT 21-JUL-1986 (Rel. 01, Last sequence update) DT 21-JUL-1986 (Rel. 01, Last annotation update) DE Eosinophilotactic peptides. S Homo saplens (Human). OC ENARIOTES (Human). ON NCBI_TAXID=9606; RN MEDLINE-76078412; PubMed=1060093; RN MEDLINE-76078412; PubMed=1060009; RN MEDLINE-76078412; PubMed=10600000; RN MEDLINE-76078412; AND OTHER PERFERMINELY AFFECTION CCC (AND OTHER PERFIRENTIALLY AFFECTION	JOSEL SIMILIATILY 100.05; PT 1 V 1 1

Gaps

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Length 5;

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TISSUE-Skin secretion;
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
"Tyler M.J., Wallow G. J.C.,
"The structure of new peptides from the Australin red tree frog
"Intoria rubella'. the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
-I- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Litoria rubella (Desert tree frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachla; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria.
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Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
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Wabbitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing
Litori electrica. Comparison with the skin peptides from
                                                                                                                         5 AA; 616 MW; 61FZD1A059A00000 CRC64;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
115-JUN-2002 (Rel. 41, Last annotation update)
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tive 0; Mismatches
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rubella.";
Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: SECRETED.
Amphibian skin; Amidation.
AMIDAT
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15-JUN-2002 (Rel. 41, Last anno
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                                                                                                                                                                                                                                         Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rubellidin 3.2
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P82070;
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                                                                                                                                                         SEQUENCE
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              STRCRES
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                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                   "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria."; FEBS Lett. 284:51-56(1991). PIR; S17255; S17255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria rubella.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wabnitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liforia rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mambildia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria.
NCBI_TaxID=104895;
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Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria
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                                                                                                                                                                                                                                                                                        100.0%; Score 4; DB 1; Length 4; larity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                   4 AA; 402 MW; 7771B2D5D000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aust. J. Chem. 52:639-645(1999).
-1- SUBCELLULAR LOCATION: SECRETED.
Amphiblan skin; Amidation.
5 5 5 AMIDATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                              Ribosomal protein; Mitochondrion.
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                                                                                                                                                SGD; L0002681; MRPL1
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Matches 1; Conserv
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Matches 1; Conserv
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        Kitakawa M.;
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P82100;
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RESULT 3 EI03_LITRU

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RESULT 4 EI04_LITRU

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tree frog Litoria

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Panicoldeae; Andropogoneae; Zea.
NCBI_TaxID-4577;
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01-MAY-1992 (Rel. 22,
15-JUN-2002 (Rel. 41,
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Best Local Similarity
Matches 1; Conserv
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                                                                                                                                                                                                                                                                                                        5 AA;
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P25154;
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NON_TER
SEQUENCE
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SEQUENCE
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     SO CC CC REPARAMENT OF THE PROPERTY OF THE PRO
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98163340; PubMed-9504812;
Dunn M.J., Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electrophoresis 18:2795-2802(1997).
-1- CATALYTIC ACTIVITY: D-91yceraldehyde 3-phosphate = glycerone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000652; Triophos_ismrse.
PROSITS: PS00171; TiM; PARTIAL.
Isomerase: Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
Pentose shunt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
rubella.";
Aust. J. Chem. 52:639-645(1999).
-1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                          -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS
                                                                                                                                                                                         Indels
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15-JUL-1998 (Rel. 36, Last annotation update)
Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
                                                                                                               5 AA; 570 MW; 71A9C9C862A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AA; 550 MW; 64444862C9A00000 CRC64;
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. 0;
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                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 34, Created)
(Rel. 34, Last seq
                                                                                                                                                                                         Conservative
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                                                                                                                                                  Query Match
Best Local Similarity
Matches 1; Conserv
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Matches 1; Conser
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                                                                                           Amphibian skin.
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P80628;
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UC22_MAIZE
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Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acylamino-acid releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
(APH) (Acylaminoacyl-peptidase) (Fragment)
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"N-terminal sequence analysis of N alpha-acetylated proteins after
unblocking with N-acylaminoacyl-peptide hydrolase.";
Anal. Blochem. 199:45-50(1991).
-I-FUNCTION: THIS ENZYME CATALZES THE HYDROLYSIS OF THE AMINO-
TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER
                                                                                     genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-I- MISCELLANEOUS: ON THE 2DE THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
Malze-2DPAGE; P80628; COLEOPTILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
Wakaryota; Metazoa; Chordata; Graniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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Pred. No. 0;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                               654 MW; 72CB19C9C0300000 CRC64;
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-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
MEROPS; S09.004; -.
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PROSITE: PS00708; PRO_ENDOPEP_SER; PARTIAL.
Hydrolase; Acetylation.
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Conservative
STANDARD;
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                                                                                       NCBI_TaxID=104895;
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-i- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y., Structures and actions of Mytilus inhibitory peptides.";
Biochem. Biophys. Res. Commun. 152:1376-1387(1988)
-1- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
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                          01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Contraction-Inhibiting peptide I (MIP I).
Wytilus edulis (Blue mussel).
Eukaryotes, Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilidae; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
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72C9C6876DD81000 CRC64;
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(Rel. 13, Last sequence update)
(Rel. 37, Last annotation update)
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Mytilus edulis (Blue mussel).
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         PRT;
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MEDLINE-88240357; PubMed-3377776;
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MEDLINE-88240357; PubMed-3377776;
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NCBI_TaxID=6550;
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-1- SIMILARITY: TO MIP I.
PIR; B27696, B27696.
Hormone; Amidation.
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        STANDARD;
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Hormone; Amidation.
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Best Local Similarity
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Best Local Similarity
      CIPI_MYTED
P13736:
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01-JAN-1990
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CIP1_MYTED
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
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                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Skin secretion;
Wabbitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resistance plasmid, pCF10.";
J. Biol. Chem. 253:14574-14578(1988).
-!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMOLYSIN PLASMID PCF10.
                                                                                                                                                                     Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mori M., Sakagami Y., Ishil Y., Isogal A., Kitada C., Fujino M., Adait J.C., Dunny G.M., Suzuki A.;
"Structure of CCFIO, a peptide sex pheromone which induces conjugative transfer of the Streptococcus faecalis tetracycline
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6 AA; 792 MW; 6683704772C9A000 CRC64;
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100.0%; Pred. No. 0;
Live 0; Mismatches
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
                        P82096;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aust. J. Chem. 52:639-645(1999).
-1- SUBCELLULAR LOCATION: SECRETED.
Amphiblan skin; Amidation.
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                                                                                     Achatina fullca (Giant African snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Achatinacea; Achatinidae; Achatina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ochatina fulica (Giant African snail).
Sukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Nchatinacea; Achatinidae; Achatina.
(NBL_TaxID=6530;
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**Mamide-1, -2 and -3: novel neuromodulatory peptides isolated from
ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
                                                                                                                                                                                                                                                                                              5 Lett. 323:104-108(1993).
FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K., Wamidel., -2 and -3: novel neuromodulatory peptides isolated from ganglia of the Arrican giant snail, Achatina fulica."; FEBS Lett. 323:104-108(1993).
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964 MW; 7362D5B686D32310 CRC64;
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7 AA; 993 MW; 7362D5B69B041310 CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
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Last annotation update)
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MEDLINE-93265912; PubMed-8495720;
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                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq
01-OCT-1994 (Rel. 30, Last anno
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MOD_RES 7 7 7 SEQUENCE 7 AA; 993 MW;
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MOD_RES 7 7 7 SEQUENCE 7 AA: 964 years
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Best Local Similarity
Matches 1; Conserv
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EDLINE=93265912;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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MEDILINE-91282758; pubMed=1840486;
Sato H., Aono S., Kashiwamata S., Kolwai O.;
Sato H., Aono S., Kashiwamata S., Kolwai O.;
Genetic defect of bilitubin UDP-glucuronosyltransferase in the hyperbilitubinemic Gunn rat.";
Blochen. Bloch
                              008485 | 008485 | 008485 | 008643 | 008628 | 008628 | 0086515 | 0086518 | 0086429 | 0086429 | 0086429 | 0086429 | 0086428 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 0083892 | 00
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT)
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Q9H4D3
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91.171 Million cell updates/sec
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                        GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Match
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Title: Perfect :

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Result

MW; 633732C42000000 CRC64;

473

4 AA;

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034028 sphingomona P70804 azotobacter 054248 streptomyce P72081 nocardia la 095545 aaccharomyc 095553 arabidopsis P93233 lycopersico

enterobacte actinobacil

Transferase; Glycosyltransferase; Microsome; Multigene family

-1- SUBCELLULAR LOCATION: MICROSOME. EMBL; S38636; AAB19259.1; -.

EMBL;

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Kraig E.;
"cis Blements and trans factors are both important in strain-specific regulation of the leukotoxin gene in Actinobacillus actinomycetemcomitans.";
Infect. Immun. 64.3451.3460(1996).
EMBL; U51862; AAB88721.1;
                                                                                                                                                                                                                                          Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
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                                                                                             Actinobacillus actinomycetemcomitans (Haemophilus actinomycetemcomitans).
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Actinobacillus.
NCBI_TaxID=714;
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U88298; AAB66311.1; -.
             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last an
Catechol-2,3-dloxygenase (Fragment)
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MEDLINE-96355846; PubMed-8751884;
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01-FEB-1997 (TIEMBLED. 02,
01-DEC-2001 (TIEMBLED. 19,
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NCBI_TaxID=56193;
                                                                GlyA (Fragment)
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01-JAN-1998 (
01-DEC-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDILINE-94079349; Pubmed-8257126;
Rather P.N., Mann P.A., Merzwa R., Hare R.S., Miller G.H., Shaw K.J.;
"Analysis of the aac(3)-Via gene encoding a novel 3-N-
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                                                                                                          01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Antimicrob. Agents Chemother. 37:2074-2079(1993).
EMBL; M88012; AAA16193.1; -.
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EMBL; AF003700; AAC35193.1; -.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
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Gapa

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"Characterization of the cmcH genes of Nocardia lactamdurans and
Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem
O-carbamoyltransferase for cephamycin biosynthesis.";
      Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
NCBI_TaxID=1913;
                                                   SEQUENCE FROM N.A.
MEDLINE-96009872; PubMed-7557411;
MEDLINE-97. Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
Liras P.;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DC-2001 (TrEMBLrel. 19, Last annotation update)
Bypothetical 0.7 kDa protein (Fragment).
DIDI 10A-2B.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.; "Assembly of the mitochondrial membrane system: Structure and nucleotide sequence of the gene coding for subunit 1 of yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                               SEQUENCE 7 AA; 746 MW; 75AIB2CDDIE681C0 CRC64;
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7 AA; 859 MW; 75B7232362CDC460 CRC64;
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100.0%; Pred. No. 6.6e+05;
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EMBL; V00694; CAA24066.1; -.
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EMBL; Z21682; CAA79797.1; -.
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"A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is part of an alg gene Cluster physically organized in a manner similar to that in pseudomonas aeruqinosa ";
J. Bacteriol. 178:5884-5889(1996).
BEMBL, SK89773; CAA61230.1;
NON TER
SEQUENCE 7 AA; 684 MW; 71B5A5A5A2DIAEDO CRC64;
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"Analysis and regulation of the sec Y gene from Streptomyces griseus N2-3-11 and interaction of the SecY protein with the SecA protein.";
Blochim. Blochim. Acta 1447:2298-302(1999).
EMBL; X95915; CAA65160.1;
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                                                 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-DEC-2001 (TrEMBLED. 19, Last annotat
3'-methylcephem hydroxylase (Fragment).
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MEDLINE=20011291; Pubmed=10542330;
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AlgT protein (Fragment)
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                                Azotobacter vinelandii
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SEQUENCE FROM N.A.
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                                                                                NCBI_TaxID=354;
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STRAIN=FS772/70;
MEDIJNE-88216185; PubMed=2835592;
Britton P., Carmenes R.S., Page K.W., Garwes D.J., Parra F.;
Britton P., Carmenes R.S., Page K.W., Garwes D.J., Parra F.;
Sequence of the Nucleoprotein Gene from a Virulent British Field
Isolate of Transmissible Gastroenteritis Virus and its Expression in
Saccharomyces Cerevisiae.";
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01-DEC-2001 (TTEMBLEEL. 19, Last annotation update)
Membrane protein (1 is.3rd base in codon) (Fragment).
Transmissible gastroenteritis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronavirus.
NOTE TRANSMISSIONERS.
                                                                                                   Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R., Wojtaszek P., Bolwell G.P.,
                                                                                                                                                                          "Proteomic study of secondary cell wall proteins from transformed
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01-NAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Llarity 100.0%; Pred. No. 6.6e+05;
Conservative 0; Mismatches 0;
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-1- TISSUE SPECIFICITY: XYLEM.
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EMBL; Y00542; CAA68606.1; -.
NON_TER ' 1
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NCBI_TaxID-4097;
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Blee K.A.,
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Octiker J.H., Olson D.C., Shlu O.Y., Yang S.F.;
Octiker J.H., olson D.C., Shlu O.Y., Yang S.F.;
"Differential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato (Lycopersicon esculentum).";
Plant Mol. Biol. 34:275-286(1997).
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum (Tomato).
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
                                                                                                                                           Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.; "Arabidopsis thaliana genes expressed in the early compatible interaction with root-knot nematodes."; Mol. Plant Microbe Interact. 14:288-299(2001).

EMBL; AJ286350; CAB71014.2;
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Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 7; 6.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
10 kDa cell wall protein (Fragment).
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7 AA; 828 MW; 71B412C7377415D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    7 AA; 719 MW; 6732C7287EB325D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 4;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                  MEDLINE-21171025; PubMed-11277426;
                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                pothetical protein
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Matches 1; Conserv
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Matches 1; Conserv
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Exawford-Miksza L.K., Nang R.N., Schnurr D.P.;
"Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=85755;
MEDLINE-99175282; PubMed-10074533; Crawford-Miksza L.K., Nang R.N., Schnurr D.P.; Strain variation in adenovirus serotypes 4 and 7a causing acute respiratory disease."

J. Clin. Microbiol. 37:1107-1112(1999).
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                                                                                                                                             STRAIN-GOMEN;
Crawford-Miksza L.K.;
Crawford-Miksza L.K.;
SULMitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065065, AAD03662.1;
NON_TER 1
SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY 1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065068; AAD03668.1; -
EMBL; AF065066; AAD03664.1; -
EMBL; AF065067; AAD03666.1; -
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
PVI core protein (Fragment).
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STRAIN-KN T96-0620,
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